```
                       SEQUENCE LISTING

<110>  Large Scale Biology
       Reinl, Stephen J.
       Edwards, Patricia C.

<120>  MULTIMERIC PROTEIN ENGINEERING

<130>  34150-004A

<150>  60/415,940
<151>  2002-10-03

<160>  122

<170>  PatentIn version 3.2

<210>  1
<211>  38
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  C-anchor, see Example 6

<400>  1
gaccacgcgt atcgatgtcg accccccccc cccccccd                            38


<210>  2
<211>  24
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  7197

<400>  2
atgaggtkcy ywsytsagyt yctg                                           24


<210>  3
<211>  28
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  2227, see Example 6

<400>  3
gtgcctaggt catttaccag gagagtgg                                       28


<210>  4
<211>  31
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  2230, see Example 5

<400>  4
gtggcatgct agacattgtg ctgacccaat c                                   31
```

```
<210>  5
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  2228, see Example 6

<400>  5
gagcctaggc taacactcat tcctgttgaa                                        30


<210>  6
<211>  42
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  6057, see Example 6

<400>  6
ctgtatcgta cgtttacctc cacactcatt cctgttgaag ct                          42


<210>  7
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  7659, see Example 6

<400>  7
gtggccggcc aaattgttct cacccagtct                                        30


<210>  8
<211>  38
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  7660, see Example 6

<400>  8
cgaggcaaga ggggaggtga ggtaaagctg gaggagtc                               38


<210>  9
<211>  31
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  7662, see Example 6

<400>  9
gtgcctaggt caacagggct tgattgtggg c                                      31


<210>  10
```

```
<211>  28
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  9E10Lngo5', see Example 15

<400>  10
gtggccggcg acattgtgct gacccaat                                        28


<210>  11
<211>  20
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  9E10L3'sr, see Example 15

<400>  11
cgtttgattt ccagcttggt                                                 20


<210>  12
<211>  23
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  9E10H5'srs, see Example 15

<400>  12
ggtgaagtag atctggttga gtc                                             23


<210>  13
<211>  18
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  9E10H3'sr, see Example 15

<400>  13
gctgaggaga cggtgact                                                   18


<210>  14
<211>  39
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  6058, see Example 5

<400>  14
cgaggcaaga ggggaggtga agtagatctg gttgagtct                            39


<210>  15
<211>  22
<212>  DNA
<213>  Artificial Sequence
```

```
<220>
<223>  KP6v23'sr , see Example 15

<400>  15
cctcctcgct ttccgatatc ag                                              22


<210>  16
<211>  33
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  HuCLv23'sr, see Example 15

<400>  16
cgcttagaca atgaacactc tcccctgttg aag                                  33


<210>  17
<211>  34
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Iggch1avr3'

<400>  17
ggtcctaggt catgtgtgag ttttgtcaca agat                                 34


<210>  18
<211>  32
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  ch1CTavr3', see Example 16

<400>  18
ggtcctaggt caacaagatt tgggctcaac tc                                   32


<210>  19
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  hCH15'sr, see Example 15

<400>  19
gcatccacca agggcccatc g                                               21


<210>  20
<211>  33
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  hCH3avr3', see Example 15
```

```
<400>  20
caccctaggt catttacccg grgacaggga gag                                    33


<210>  21
<211>  20
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  HuCL5'sr, see Example 15

<400>  21
cgaactgtgg ctgcaccatc                                                   20


<210>  22
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  HuCL3'sr, See Example 15

<400>  22
cgcttacctc cacactctcc cctgttgaag                                        30


<210>  23
<211>  20
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  KP6v15'sr, see Example 16

<400>  23
gcgtacgata caggattctg                                                   20


<210>  24
<211>  17
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  KP6v13'sr, see Example 15

<400>  24
cctcccctct tgcctcg                                                      17


<210>  25
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  hCHC2avr3', see Example 15

<400>  25
gtgcctaggt cagcacggtg ggcatgtgtg                                        30
```

```
<210>  26
<211>  25
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  natKp6Nt3', see Example 16

<400>  26
cgcttacact ctcccctgtt gaagc                                              25


<210>  27
<211>  31
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  natKp6Ct5', see Example 16

<400>  27
cggaaagcga gaagtagatc tggttgagtc t                                       31


<210>  28
<211>  20
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  natKp6Ct3', see Example 16

<400>  28
ccgatatcag aagcagtagg                                                    20


<210>  29
<211>  35
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  5230, see Example 2

<400>  29
ggtggttaat taacatggac atgagggtcc cygct                                   35


<210>  30
<211>  38
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  5233, see Example 2

<400>  30
cagacgcggc cgctcatgtg tgagttttgt cacaagat                                38


<210>  31
```

```
<211>  41
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  5235, see Example 2

<400>  31
ctgtatcgta cgtttacctt ccacactctc ccctgttgaa g                           41


<210>  32
<211>  36
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  5236, see Example 2

<400>  32
cgaggcaaga ggggaggtsa ggtgcagctg gtggag                                 36


<210>  33
<211>  47
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  KP6-5', see Example 1

<400>  33
gctcttcaaa cgtacgatac aggattctgc aactgataca gttgact                     47


<210>  34
<211>  56
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  KP6-c3', see Example 1

<400>  34
gtaggtggag ggtcatctct tgcaactctg cacctagtca actgtatcag ttgcag           56


<210>  35
<211>  49
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  KP6-3' , see Example 1

<400>  35
gctcttcctc gctttccgat atcagaagca gtaggtggag ggtcatctc                   49


<210>  36
<211>  28
<212>  DNA
<213>  Artificial Sequence
```

<220>
<223> 5228, see Example 1

<400> 36
ggaggtaaac gtacgataca ggattctg 28

<210> 37
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> 5229, see Example 1

<400> 37
acctcccctc ttgcctcgct ttccgatatc aga 33

<210> 38
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> 5609, see Example 2

<400> 38
cagacgcggc cgctca 16

<210> 39
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> 2225, see Example 4

<400> 39
gtggcatgct agaagtagat ctggttgagt ctgg 34

<210> 40
<211> 40
<212> DNA
<213> Artificial Sequene

<220>
<223> 6055, see Example 4

<400> 40
ctgtatcgta cgtttacctc caccacaatc cctgggcaca 40

<210> 41
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> 6056, see Example 4

<400> 41
cgaggcaaga ggggaggtga cattgtgctg acccaatc 38

<210> 42
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> 4D5 HySph5', see Example 11

<400> 42
ggtgcatgca ggttcagctg cagcagtct 29

<210> 43
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> 4D5 LtSph5', see Example 11

<400> 43
ggtgcatgct tgatatcgtg atgacccagt c 31

<210> 44
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> 4D5HyKp63', see Example 12

<400> 44
ctgtatcgta cgtttacctc caccacaatc cctgggcaca at 42

<210> 45
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> 4D5LtKp65', see Example 12

<400> 45
cgaggcaaga ggggaggtga tatcgtgatg acccagtc 38

<210> 46
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> 4D5LtKp63', see Example 13

<400> 46
ctgtatcgta cgtttacctc cacactcatt cctgttgaag ct 42

```
<210>  47
<211>  39
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  4D5HyKp65', see Example 13

<400>  47
cgaggcaaga ggggaggtca ggttcagctg cagcagtct                              39


<210>  48
<211>  33
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  4D5Havstp3', see Example 13

<400>  48
ggtcctaggt caaccacaat ccctgggcac aat                                    33


<210>  49
<211>  33
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  4D5Lavstp3', see Example 12

<400>  49
ggtcctaggt caacactcat tcctgttgaa gct                                    33


<210>  50
<211>  22
<212>  DNA
<213>  Murine  [9E10kl5', Example 3]

<400>  50
atggagacag acacactcct gc                                                22


<210>  51
<211>  22
<212>  DNA
<213>  Murine  [9E10gfw5', Example 3]

<400>  51
gacatcgtac tcacacagtc tc                                                22


<210>  52
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  4D5 Hy Avr3', see Example 11
```

```
<400>  52
ggtcctagga ccacaatccc tgggcacaat                                      30


<210>  53
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  4D5 Lt Avr3', see Example 11

<400>  53
ggtcctagga cactcattcc tgttgaagct                                      30


<210>  54
<211>  19
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  5696s , see Example 14

<400>  54
aggctactgt cgccgaatc                                                  19


<210>  55
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  4D5fAb3' , see Example 14

<400>  55
ggaacaattt tcttgtccac cttggtg                                         27


<210>  56
<211>  24
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  9E10Fc5' , see Example 14

<400>  56
ccaagggatt gtggttgtaa gcct                                            24


<210>  57
<211>  1002
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  phCHTOPO , see Example 15

<400>  57
gcatccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg     60
```

```
ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg     120
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca     180
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc     240
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc     300
aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga     360
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct     420
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg     480
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac     540
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag     600
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc     660
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag     720
ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc     780
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg     840
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg     900
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg     960
cagaagagcc tctccctgtc tccgggtaaa tgacctaggg tg                      1002
```

<210> 58
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> PhCHTOPO, see Example 15

<400> 58

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1               5                   10                  15


Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30


Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45


Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60


Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80
```

```
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115                 120                 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225                 230                 235                 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305                 310                 315                 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
```

```
<210>  59
<211>  321
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  huscFabm1A6 , see Example 15

<400>  59
cgaactgtgg ctgcaccatc tgtcttcatc ttcccgccat ctgatgagca gttgaaatct      60

ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag     120

tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac     180

agcaaggaca gcacctacag cctcagcagc accctgacgc tgagcaaagc agactacgag     240

aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag     300

agcttcaaca ggggagagtg t                                               321


<210>  60
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  huscFabm1A6 , see Example 15

<400>  60

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1               5                   10                  15


Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
            20                  25                  30


Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        35                  40                  45


Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
    50                  55                  60


Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65                  70                  75                  80


Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
                85                  90                  95


Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            100                 105


<210>  61
```

<211> 2160
<212> DNA
<213> Artificial Sequence

<220>
<223> p9E10chimericv1-1, see Example 15

<400> 61
gccggcgaca ttgtgctgac ccaatctcca gcttctttgg ctgtatctct aggacagagg 60

gccaccatct cctgcagagc cagcgaaagt gttgataatt atggctttag ttttatgaac 120

tggttccaac agaaaccagg acagccaccc aaactcctca tctatgctat atccaaccga 180

ggatccgggg tccctgccag gtttagtggc agtgggtctg ggacagactt cagcctcaac 240

atccatcctg tagaggagga tgatcctgca atgtatttct gtcagcaaac taaggaggtt 300

ccgtggacgt tcggtggagg caccaagctg gaaatcaaac gaactgtggc tgcaccatct 360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

ggaggtaagc gtacgataca ggattctgca actgatacag ttgacttagg tgcagagttg 720

catagagatg accctccacc tactgcttct gatatcggaa agcgaggcaa gaggggaggt 780

gaagtagatc tggttgagtc tgggggagac ttagtgaagc ctggagggtc cctgaaactc 840

tcctgtgcag cctctggatt cactttcagt cactatggca tgtcttgggt tcgccagact 900

ccagacaaga ggctggagtg ggtcgcaacc attggtagtc gtggtactta cacccactat 960

ccagacagtg tgaagggacg attcaccatc tccagagaca atgacaagaa cgccctgtac 1020

ctgcaaatga acagtctgaa gtctgaagac acagccatgt attactgtgc aagaagaagt 1080

gaattttatt actacggtaa tacctactat tactctgcta tggactactg gggtcaagga 1140

gcctcagtca ccgtctcctc agcatccacc aagggcccat cggtcttccc cctggcaccc 1200

tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctggtcaa ggactacttc 1260

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 1320

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 1380

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 1440

gtggacaaga gagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 1500

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 1560

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 1620

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1680

```
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac    1740

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc    1800

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc    1860

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa    1920

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac    1980

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc    2040

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag    2100

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atgacctagg    2160
```

```
<210>  62
<211>  715
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  p9E10chimericv1-1, see Example 15

<400>  62
```

```
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Asn Tyr
            20                  25                  30


Gly Phe Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45


Lys Leu Leu Ile Tyr Ala Ile Ser Asn Arg Gly Ser Gly Val Pro Ala
    50                  55                  60


Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His
65                  70                  75                  80


Pro Val Glu Glu Asp Asp Pro Ala Met Tyr Phe Cys Gln Gln Thr Lys
                85                  90                  95


Glu Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105                 110


Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
        115                 120                 125


Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
    130                 135                 140
```

```
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145                 150                 155                 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                165                 170                 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
            180                 185                 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
        195                 200                 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Gly Lys Arg Thr Ile
    210                 215                 220

Gln Asp Ser Ala Thr Asp Thr Val Asp Leu Gly Ala Glu Leu His Arg
225                 230                 235                 240

Asp Asp Pro Pro Pro Thr Ala Ser Asp Ile Gly Lys Arg Gly Lys Arg
                245                 250                 255

Gly Gly Glu Val Asp Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro
            260                 265                 270

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
        275                 280                 285

His Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu
    290                 295                 300

Trp Val Ala Thr Ile Gly Ser Arg Gly Thr Tyr Thr His Tyr Pro Asp
305                 310                 315                 320

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Asp Lys Asn Ala
                325                 330                 335

Leu Tyr Leu Gln Met Asn Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr
            340                 345                 350

Tyr Cys Ala Arg Arg Ser Glu Phe Tyr Tyr Tyr Gly Asn Thr Tyr Tyr
        355                 360                 365

Tyr Ser Ala Met Asp Tyr Trp Gly Gln Gly Ala Ser Val Thr Val Ser
    370                 375                 380

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
385                 390                 395                 400
```

```
Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
                405                 410                 415

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
            420                 425                 430

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
        435                 440                 445

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
    450                 455                 460

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
465                 470                 475                 480

Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
                485                 490                 495

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
            500                 505                 510

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
        515                 520                 525

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
    530                 535                 540

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
545                 550                 555                 560

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
                565                 570                 575

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
            580                 585                 590

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
        595                 600                 605

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
    610                 615                 620

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
625                 630                 635                 640

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
```

645 650 655

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
660 665 670

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
675 680 685

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
690 695 700

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
705 710 715

<210> 63
<211> 2154
<212> DNA
<213> Artificial Sequence

<220>
<223> p9E10chimericv2-1, see Example 15

<400> 63
gccggcgaca ttgtgctgac ccaatctcca gcttctttgg ctgtatctct aggacagagg 60

gccaccatct cctgcagagc cagcgaaagt gttgataatt atggctttag ttttatgaac 120

tggttccaac agaaaccagg acagccaccc aaactcctca tctatgctat atccaaccga 180

ggatccgggg tccctgccag gtttagtggc agtgggtctg ggacagactt cagcctcaac 240

atccatcctg tagaggagga tgatcctgca atgtatttct gtcagcaaac taaggaggtt 300

ccgtggacgt tcggtggagg caccaagctg gaaatcaaac gaactgtggc tgcaccatct 360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

tcattatcta agcgtacgat acaggattct gcaactgata cagttgactt aggtgcagag 720

ttgcatagag atgaccctcc acctactgct tctgatatcg gaaagcgagg aggtgaagta 780

gatctggttg agtctggggg agacttagtg aagcctggag ggtccctgaa actctcctgt 840

gcagcctctg gattcacttt cagtcactat ggcatgtctt gggttcgcca gactccagac 900

aagaggctgg agtgggtcgc aaccattggt agtcgtggta cttacaccca ctatccagac 960

agtgtgaagg gacgattcac catctccaga gacaatgaca agaacgccct gtacctgcaa 1020

atgaacagtc tgaagtctga agacacagcc atgtattact gtgcaagaag aagtgaattt 1080

```
tattactacg gtaataccta ctattactct gctatggact actggggtca aggagcctca    1140

gtcaccgtct cctcagcatc caccaagggc ccatcggtct tccccctggc accctcctcc    1200

aagagcacct ctgggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa    1260

ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct    1320

gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc    1380

ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac    1440

aagagagttg agcccaaatc ttgtgacaaa actcacacat gcccaccgtg cccagcacct    1500

gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg    1560

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag    1620

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg    1680

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac    1740

tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc agcccccatc    1800

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc    1860

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc    1920

tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag    1980

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg    2040

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg    2100

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaatgacc tagg          2154
```

```
<210>  64
<211>  713
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  p9E10chimericv2-1, see Example 15

<400>  64

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Asn Tyr
            20                  25                  30


Gly Phe Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45


Lys Leu Leu Ile Tyr Ala Ile Ser Asn Arg Gly Ser Gly Val Pro Ala
    50                  55                  60
```

```
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His
65                  70                  75                  80

Pro Val Glu Glu Asp Asp Pro Ala Met Tyr Phe Cys Gln Gln Thr Lys
                85                  90                  95

Glu Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105                 110

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
        115                 120                 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
    130                 135                 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145                 150                 155                 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                165                 170                 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
            180                 185                 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
        195                 200                 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Ser Leu Ser Lys Arg Thr
    210                 215                 220

Ile Gln Asp Ser Ala Thr Asp Thr Val Asp Leu Gly Ala Glu Leu His
225                 230                 235                 240

Arg Asp Asp Pro Pro Pro Thr Ala Ser Asp Ile Gly Lys Arg Gly Gly
                245                 250                 255

Glu Val Asp Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
            260                 265                 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr
        275                 280                 285

Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Trp Val
    290                 295                 300

Ala Thr Ile Gly Ser Arg Gly Thr Tyr Thr His Tyr Pro Asp Ser Val
305                 310                 315                 320
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Asp Lys Asn Ala Leu Tyr
                325                 330                 335

Leu Gln Met Asn Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
            340                 345                 350

Ala Arg Arg Ser Glu Phe Tyr Tyr Tyr Gly Asn Thr Tyr Tyr Tyr Ser
        355                 360                 365

Ala Met Asp Tyr Trp Gly Gln Gly Ala Ser Val Thr Val Ser Ser Ala
    370                 375                 380

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
385                 390                 395                 400

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
                405                 410                 415

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
            420                 425                 430

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
        435                 440                 445

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
    450                 455                 460

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg
465                 470                 475                 480

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
                485                 490                 495

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            500                 505                 510

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        515                 520                 525

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    530                 535                 540

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
545                 550                 555                 560

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
```

```
                565                 570                 575

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            580                 585                 590

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        595                 600                 605

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    610                 615                 620

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
625                 630                 635                 640

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                645                 650                 655

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            660                 665                 670

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        675                 680                 685

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    690                 695                 700

Lys Ser Leu Ser Leu Ser Pro Gly Lys
705                 710


<210>  65
<211>  1572
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  pLSBC2511 , see Example 16

<400>  65
gccggcatgc aggtgctgaa caccatggtg aacaaacact tcttgtccct ttcggtcctc      60

atcgtcctcc ttggcctctc ctccaacttg acagccggcg acattgtgct gacccaatct     120

ccagcttctt tggctgtatc tctaggacag agggccacca tctcctgcag agccagcgaa     180

agtgttgata attatggctt tagttttatg aactggttcc aacagaaacc aggacagcca     240

cccaaactcc tcatctatgc tatatccaac cgaggatccg gggtccctgc caggtttagt     300

ggcagtgggt ctgggacaga cttcagcctc aacatccatc ctgtagagga ggatgatcct     360

gcaatgtatt tctgtcagca aactaaggag gttccgtgga cgttcggtgg aggcaccaag     420

ctggaaatca aacgaactgt ggctgcacca tctgtcttca tcttcccgcc atctgatgag     480
```

```
cagttgaaat ctggaactgc ctctgttgtg tgcctgctga ataacttcta tcccagagag    540

gccaaagtac agtggaaggt ggataacgcc ctccaatcgg gtaactccca ggagagtgtc    600

acagagcagg acagcaagga cagcacctac agcctcagca gcaccctgac gctgagcaaa    660

gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg    720

cccgtcacaa agagcttcaa caggggagag tgtggaggta agcgtacgat acaggattct    780

gcaactgata cagttgactt aggtgcagag ttgcatagag atgaccctcc acctactgct    840

tctgatatcg gaaagcgagg caagagggga ggtgaagtag atctggttga gtctggggga    900

gacttagtga agcctggagg gtccctgaaa ctctcctgtg cagcctctgg attcactttc    960

agtcactatg gcatgtcttg ggttcgccag actccagaca agaggctgga gtgggtcgca   1020

accattggta gtcgtggtac ttacacccac tatccagaca gtgtgaaggg acgattcacc   1080

atctccagag acaatgacaa gaacgccctg tacctgcaaa tgaacagtct gaagtctgaa   1140

gacacagcca tgtattactg tgcaagaaga agtgaatttt attactacgg taatacctac   1200

tattactctg ctatggacta ctggggtcaa ggagcctcag tcaccgtctc ctcagcatcc   1260

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca   1320

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac   1380

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc   1440

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc   1500

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaatct   1560

tgttgaccta gg                                                       1572


<210>  66
<211>  519
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  pLSBC2511 , see Example 16

<400>  66

Met Gln Val Leu Asn Thr Met Val Asn Lys His Phe Leu Ser Leu Ser
1               5                   10                  15


Val Leu Ile Val Leu Leu Gly Leu Ser Ser Asn Leu Thr Ala Gly Asp
            20                  25                  30


Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln
        35                  40                  45


Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Asn Tyr Gly
```

```
    50                  55                  60


Phe Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro Lys
65                  70                  75                  80


Leu Leu Ile Tyr Ala Ile Ser Asn Arg Gly Ser Gly Val Pro Ala Arg
                85                  90                  95


Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His Pro
            100                 105                 110


Val Glu Glu Asp Asp Pro Ala Met Tyr Phe Cys Gln Gln Thr Lys Glu
        115                 120                 125


Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr
    130                 135                 140


Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
145                 150                 155                 160


Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
                165                 170                 175


Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
            180                 185                 190


Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
        195                 200                 205


Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
    210                 215                 220


Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
225                 230                 235                 240


Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Gly Lys Arg Thr Ile Gln
                245                 250                 255


Asp Ser Ala Thr Asp Thr Val Asp Leu Gly Ala Glu Leu His Arg Asp
            260                 265                 270


Asp Pro Pro Pro Thr Ala Ser Asp Ile Gly Lys Arg Gly Lys Arg Gly
        275                 280                 285


Gly Glu Val Asp Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly
    290                 295                 300
```

```
Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His
305                 310                 315                 320


Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Trp
                325                 330                 335


Val Ala Thr Ile Gly Ser Arg Gly Thr Tyr Thr His Tyr Pro Asp Ser
            340                 345                 350


Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Asp Lys Asn Ala Leu
        355                 360                 365


Tyr Leu Gln Met Asn Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr
    370                 375                 380


Cys Ala Arg Arg Ser Glu Phe Tyr Tyr Tyr Gly Asn Thr Tyr Tyr Tyr
385                 390                 395                 400


Ser Ala Met Asp Tyr Trp Gly Gln Gly Ala Ser Val Thr Val Ser Ser
                405                 410                 415


Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
            420                 425                 430


Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
        435                 440                 445


Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
    450                 455                 460


Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
465                 470                 475                 480


Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
                485                 490                 495


Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
            500                 505                 510


Arg Val Glu Pro Lys Ser Cys
        515


<210>  67
<211>  1566
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  pLSBC2512 , see Example 16
```

<400> 67
gccggcatgc aggtgctgaa caccatggtg aacaaacact tcttgtccct ttcggtcctc 60

atcgtcctcc ttggcctctc ctccaacttg acagccggcg acattgtgct gacccaatct 120

ccagcttctt tggctgtatc tctaggacag agggccacca tctcctgcag agccagcgaa 180

agtgttgata attatggctt tagttttatg aactggttcc aacagaaacc aggacagcca 240

cccaaactcc tcatctatgc tatatccaac cgaggatccg gggtccctgc caggtttagt 300

ggcagtgggt ctgggacaga cttcagcctc aacatccatc ctgtagagga ggatgatcct 360

gcaatgtatt tctgtcagca aactaaggag gttccgtgga cgttcggtgg aggcaccaag 420

ctggaaatca aacgaactgt ggctgcacca tctgtcttca tcttcccgcc atctgatgag 480

cagttgaaat ctggaactgc ctctgttgtg tgcctgctga ataacttcta tcccagagag 540

gccaaagtac agtggaaggt ggataacgcc ctccaatcgg gtaactccca ggagagtgtc 600

acagagcagg acagcaagga cagcacctac agcctcagca gcaccctgac gctgagcaaa 660

gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg 720

cccgtcacaa agagcttcaa caggggagag tgttcattat ctaagcgtac gatacaggat 780

tctgcaactg atacagttga cttaggtgca gagttgcata gagatgaccc tccacctact 840

gcttctgata tcggaaagcg aggaggtgaa gtagatctgg ttgagtctgg gggagactta 900

gtgaagcctg gagggtccct gaaactctcc tgtgcagcct ctggattcac tttcagtcac 960

tatggcatgt cttgggttcg ccagactcca gacaagaggc tggagtgggt cgcaaccatt 1020

ggtagtcgtg gtacttacac ccactatcca gacagtgtga agggacgatt caccatctcc 1080

agagacaatg acaagaacgc cctgtacctg caaatgaaca gtctgaagtc tgaagacaca 1140

gccatgtatt actgtgcaag aagaagtgaa ttttattact acggtaatac ctactattac 1200

tctgctatgg actactgggg tcaaggagcc tcagtcaccg tctcctcagc atccaccaag 1260

ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 1320

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 1380

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 1440

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 1500

gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgttga 1560

cctagg 1566

<210> 68
<211> 517
<212> PRT
<213> Artificial Sequence

<220>

```
<223>  pLSBC2512 , see Example 16

<400>  68

Met Gln Val Leu Asn Thr Met Val Asn Lys His Phe Leu Ser Leu Ser
1               5                   10                  15


Val Leu Ile Val Leu Leu Gly Leu Ser Ser Asn Leu Thr Ala Gly Asp
            20                  25                  30


Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln
        35                  40                  45


Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Asn Tyr Gly
    50                  55                  60


Phe Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro Lys
65                  70                  75                  80


Leu Leu Ile Tyr Ala Ile Ser Asn Arg Gly Ser Gly Val Pro Ala Arg
                85                  90                  95


Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His Pro
            100                 105                 110


Val Glu Glu Asp Asp Pro Ala Met Tyr Phe Cys Gln Gln Thr Lys Glu
        115                 120                 125


Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr
    130                 135                 140


Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
145                 150                 155                 160


Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
                165                 170                 175


Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
            180                 185                 190


Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
        195                 200                 205


Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
    210                 215                 220


Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
225                 230                 235                 240
```

```
Thr Lys Ser Phe Asn Arg Gly Glu Cys Ser Leu Ser Lys Arg Thr Ile
                245                 250                 255

Gln Asp Ser Ala Thr Asp Thr Val Asp Leu Gly Ala Glu Leu His Arg
            260                 265                 270

Asp Asp Pro Pro Pro Thr Ala Ser Asp Ile Gly Lys Arg Gly Gly Glu
        275                 280                 285

Val Asp Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly Ser
    290                 295                 300

Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr Gly
305                 310                 315                 320

Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Trp Val Ala
                325                 330                 335

Thr Ile Gly Ser Arg Gly Thr Tyr Thr His Tyr Pro Asp Ser Val Lys
            340                 345                 350

Gly Arg Phe Thr Ile Ser Arg Asp Asn Asp Lys Asn Ala Leu Tyr Leu
        355                 360                 365

Gln Met Asn Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys Ala
    370                 375                 380

Arg Arg Ser Glu Phe Tyr Tyr Tyr Gly Asn Thr Tyr Tyr Tyr Ser Ala
385                 390                 395                 400

Met Asp Tyr Trp Gly Gln Gly Ala Ser Val Thr Val Ser Ser Ala Ser
                405                 410                 415

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
            420                 425                 430

Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
        435                 440                 445

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
    450                 455                 460

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
465                 470                 475                 480

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
                485                 490                 495
```

```
Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val
            500                 505                 510


Glu Pro Lys Ser Cys
        515
```

<210> 69
<211> 1551
<212> DNA
<213> Artificial Sequence

<220>
<223> pLSBC2514, see Example 16

<400> 69
gccggcatgc aggtgctgaa caccatggtg aacaaacact tcttgtccct ttcggtcctc 60

atcgtcctcc ttggcctctc ctccaacttg acagccggcg acattgtgct gacccaatct 120

ccagcttctt tggctgtatc tctaggacag agggccacca tctcctgcag agccagcgaa 180

agtgttgata attatggctt tagttttatg aactggttcc aacagaaacc aggacagcca 240

cccaaactcc tcatctatgc tatatccaac cgaggatccg gggtccctgc caggtttagt 300

ggcagtgggt ctgggacaga cttcagcctc aacatccatc ctgtagagga ggatgatcct 360

gcaatgtatt tctgtcagca aactaaggag gttccgtgga cgttcggtgg aggcaccaag 420

ctggaaatca aacgaactgt ggctgcacca tctgtcttca tcttcccgcc atctgatgag 480

cagttgaaat ctggaactgc ctctgttgtg tgcctgctga ataacttcta tcccagagag 540

gccaaagtac agtggaaggt ggataacgcc ctccaatcgg gtaactccca ggagagtgtc 600

acagagcagg acagcaagga cagcacctac agcctcagca gcaccctgac gctgagcaaa 660

gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg 720

cccgtcacaa agagcttcaa caggggagag tgtaagcgta cgatacagga ttctgcaact 780

gatacagttg acttaggtgc agagttgcat agagatgacc ctccacctac tgcttctgat 840

atcggaaagc gagaagtaga tctggttgag tctgggggag acttagtgaa gcctggaggg 900

tccctgaaac tctcctgtgc agcctctgga ttcactttca gtcactatgg catgtcttgg 960

gttcgccaga ctccagacaa gaggctggag tgggtcgcaa ccattggtag tcgtggtact 1020

tacacccact atccagacag tgtgaaggga cgattcacca tctccagaga caatgacaag 1080

aacgccctgt acctgcaaat gaacagtctg aagtctgaag acacagccat gtattactgt 1140

gcaagaagaa gtgaatttta ttactacggt aatacctact attactctgc tatggactac 1200

tggggtcaag gagcctcagt caccgtctcc tcagcatcca ccaagggccc atcggtcttc 1260

cccctggcac cctcctccaa gagcacctct gggggcacag cggccctggg ctgcctggtc 1320

```
aaggactact tccccgaacc ggtgacggtg tcgtggaact caggcgccct gaccagcggc   1380

gtgcacacct tcccggctgt cctacagtcc tcaggactct actccctcag cagcgtggtg   1440

accgtgccct ccagcagctt gggcacccag acctacatct gcaacgtgaa tcacaagccc   1500

agcaacacca aggtggacaa gagagttgag cccaaatctt gttgacctag g            1551
```

<210> 70
<211> 512
<212> PRT
<213> Artificial Sequence

<220>
<223> pLSBC2514 , see Example 16

<400> 70

```
Met Gln Val Leu Asn Thr Met Val Asn Lys His Phe Leu Ser Leu Ser
1               5                   10                  15


Val Leu Ile Val Leu Leu Gly Leu Ser Ser Asn Leu Thr Ala Gly Asp
            20                  25                  30


Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln
        35                  40                  45


Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Asn Tyr Gly
    50                  55                  60


Phe Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro Lys
65                  70                  75                  80


Leu Leu Ile Tyr Ala Ile Ser Asn Arg Gly Ser Gly Val Pro Ala Arg
                85                  90                  95


Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His Pro
            100                 105                 110


Val Glu Glu Asp Asp Pro Ala Met Tyr Phe Cys Gln Gln Thr Lys Glu
        115                 120                 125


Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr
    130                 135                 140


Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
145                 150                 155                 160


Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
                165                 170                 175
```

```
Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
            180                 185                 190

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
        195                 200                 205

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
    210                 215                 220

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
225                 230                 235                 240

Thr Lys Ser Phe Asn Arg Gly Glu Cys Lys Arg Thr Ile Gln Asp Ser
                245                 250                 255

Ala Thr Asp Thr Val Asp Leu Gly Ala Glu Leu His Arg Asp Asp Pro
            260                 265                 270

Pro Pro Thr Ala Ser Asp Ile Gly Lys Arg Glu Val Asp Leu Val Glu
        275                 280                 285

Ser Gly Gly Asp Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys
    290                 295                 300

Ala Ala Ser Gly Phe Thr Phe Ser His Tyr Gly Met Ser Trp Val Arg
305                 310                 315                 320

Gln Thr Pro Asp Lys Arg Leu Glu Trp Val Ala Thr Ile Gly Ser Arg
                325                 330                 335

Gly Thr Tyr Thr His Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile
            340                 345                 350

Ser Arg Asp Asn Asp Lys Asn Ala Leu Tyr Leu Gln Met Asn Ser Leu
        355                 360                 365

Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys Ala Arg Arg Ser Glu Phe
    370                 375                 380

Tyr Tyr Tyr Gly Asn Thr Tyr Tyr Tyr Ser Ala Met Asp Tyr Trp Gly
385                 390                 395                 400

Gln Gly Ala Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
                405                 410                 415

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
            420                 425                 430
```

```
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
        435                 440                 445


Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
    450                 455                 460


Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
465                 470                 475                 480


Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
                485                 490                 495


Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
            500                 505                 510


<210>  71
<211>  1445
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  pLSBC1740 , see Example 12

<400>  71
gcatgcaggt tcagctgcag cagtctgggc cagagcttgt gaagccaggg gcctcactca      60

agttgtcctg tacagcttct ggcttcaaca ttaaagacac ctatatacac tgggtgaaac     120

agaggcctga acagggcctg gaatggattg gaaggattta tcctacgaat ggttatacta     180

gatatgaccc gaagttccag gacaaggcca ctataacagc agacacatcc tccaacacag     240

cctacctgca ggtcagccgc ctgacatctg aggacactgc cgtctattat tgttctagat     300

ggggagggga cggcttctat gctatggact actggggtca aggagcctca gtcaccgtct     360

cctcagccaa aacgacaccc ccatctgtct atccactggc ccctggrtct gctgcccaaa     420

ctaactccat ggtgaccctg ggatgcctgg tcaagggcta tttccctgag ccagtgacag     480

tgacctggaa ctctggatcc ctgtccagcg gtgtgcacac cttcccagct gtcctgcagt     540

ctgacctcta cactctgagc agctcagtga ctgtcccctc cagcacctgg cccagcgaga     600

ccgtcacctg caacgttgcc cacccggcca gcagcaccaa ggtggacaag aaaattgtgc     660

ccagggattg tggtggaggt aaacgtacga tacaggattc tgcaactgat acagttgact     720

taggtgcaga gttgcataga gatgaccctc cacctactgc ttctgatatc ggaaagcgag     780

gcaagagggg aggtgatatc gtgatgaccc agtctcacaa attcatgtcc acatcagtag     840

gagacagggt cagcatcacc tgcaaggcca gtcaggatgt gaatactgct gtagcctggt     900

atcaacagaa accaggacat tctccgaaac tactgattta ctcggcatcc ttccggtaca     960

ctggagtccc tgatcgcttc actggcaata gatctgggac ggatttcact ttcaccatca    1020
```

```
gcagtgtgca ggctgaagac ctggcagttt attactgtca gcaacattat actactcctc    1080

ccacgttcgg agggggggacc aagctggaga taaaacgggc tgatgctgca ccaactgtat    1140

ccatcttccc accatccagt gagcagttaa catctggagg tgcctcagtc gtgtgcttct    1200

tgaacaactt ctaccccaaa gacatcaatg tcaagtggaa gattgatggc agtgaacgac    1260

aaaatggcgt cctgaacagt tggactgatc aggacagcaa agacagcacc tacagcatga    1320

gcagcaccct cacgttgacc aaggacgagt atgaacgaca taacagctat acctgtgagg    1380

ccactcacaa gacatcaact tcacccattg tcaagagctt caacaggaat gagtgttagc    1440

ctagg                                                                1445


<210>  72
<211>  478
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  pLSBC1740 , see Example 12

<400>  72

Met Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly
1               5                   10                  15


Ala Ser Leu Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp
            20                  25                  30


Thr Tyr Ile His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp
        35                  40                  45


Ile Gly Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Asp Pro Lys
    50                  55                  60


Phe Gln Asp Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala
65                  70                  75                  80


Tyr Leu Gln Val Ser Arg Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr
                85                  90                  95


Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Ala Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser
        115                 120                 125


Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val
    130                 135                 140
```

```
Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro
            180                 185                 190

Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro
        195                 200                 205

Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly
    210                 215                 220

Gly Gly Lys Arg Thr Ile Gln Asp Ser Ala Thr Asp Thr Val Asp Leu
225                 230                 235                 240

Gly Ala Glu Leu His Arg Asp Asp Pro Pro Pro Thr Ala Ser Asp Ile
                245                 250                 255

Gly Lys Arg Gly Lys Arg Gly Gly Asp Ile Val Met Thr Gln Ser His
            260                 265                 270

Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys
        275                 280                 285

Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro
    290                 295                 300

Gly His Ser Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Arg Tyr Thr
305                 310                 315                 320

Gly Val Pro Asp Arg Phe Thr Gly Asn Arg Ser Gly Thr Asp Phe Thr
                325                 330                 335

Phe Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys
            340                 345                 350

Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
        355                 360                 365

Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
    370                 375                 380

Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
385                 390                 395                 400
```

```
Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
                405                 410                 415

Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
            420                 425                 430

Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
        435                 440                 445

Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr
    450                 455                 460

Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
465                 470                 475


<210>  73
<211>  11222
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  pLSBC1741 , see Example 13

<400>  73
gtatttttac aacaattacc aacaacaaca aacaacaaac aacattacaa ttactattta      60

caattacaat ggcatacaca cagacagcta ccacatcagc tttgctggac actgtccgag     120

gaaacaactc cttggtcaat gatctagcaa agcgtcgtct ttacgacaca gcggttgaag     180

agtttaacgc tcgtgaccgc aggcccaagg tgaacttttc aaaagtaata agcgaggagc     240

agacgcttat tgctacccgg gcgtatccag aattccaaat tacattttat aacacgcaaa     300

atgccgtgca ttcgcttgca ggtggattgc gatctttaga actggaatat ctgatgatgc     360

aaattcccta cggatcattg acttatgaca taggcgggaa ttttgcatcg catctgttca     420

agggacgagc atatgtacac tgctgtatgc ccaacctgga cgttcgagac atcatgcggc     480

acgaaggcca gaaagacagt attgaactat acctttctag gctagagaga ggggggaaaa     540

cagtccccaa cttccaaaag gaagcatttg acagatacgc agaaattcct gaagacgctg     600

tctgtcacaa tactttccag acaatgcgac atcagccgat gcagcaatca ggcagagtgt     660

atgccattgc gctacacagc atatatgaca taccagccga tgagttcggg gcggcactct     720

tgaggaaaaa tgtccatacg tgctatgccg ctttccactt ctctgagaac ctgcttcttg     780

aagattcata cgtcaatttg gacgaaatca acgcgtgttt ttcgcgcgat ggagacaagt     840

tgaccttttc ttttgcatca gagagtactc ttaattattg tcatagttat tctaatattc     900

ttaagtatgt gtgcaaaact tacttcccgg cctctaatag agaggtttac atgaaggagt     960
```

ttttagtcac cagagttaat acctggtttt gtaagttttc tagaatagat acttttcttt 1020

tgtacaaagg tgtggcccat aaaagtgtag atagtgagca gttttatact gcaatggaag 1080

acgcatggca ttacaaaaag actcttgcaa tgtgcaacag cgagagaatc ctccttgagg 1140

attcatcatc agtcaattac tggtttccca aaatgaggga tatggtcatc gtaccattat 1200

tcgacatttc tttggagact agtaagagga cgcgcaagga agtcttagtg tccaaggatt 1260

tcgtgtttac agtgcttaac cacattcgaa cataccaggc gaaagctctt acatacgcaa 1320

atgttttgtc ctttgtcgaa tcgattcgat cgagggtaat cattaacggt gtgacagcga 1380

ggtccgaatg ggatgtggac aaatctttgt tacaatcctt gtccatgacg ttttacctgc 1440

atactaagct tgccgttcta aaggatgact tactgattag caagtttagt ctcggttcga 1500

aaacggtgtg ccagcatgtg tgggatgaga tttcgctggc gtttgggaac gcatttccct 1560

ccgtgaaaga gaggctcttg aacaggaaac ttatcagagt ggcaggcgac gcattagaga 1620

tcagggtgcc tgatctatat gtgaccttcc acgacagatt agtgactgag tacaaggcct 1680

ctgtggacat gcctgcgctt gacattagga agaagatgga agaaacggaa gtgatgtaca 1740

atgcactttc agagttatcg gtgttaaggg agtctgacaa attcgatgtt gatgtttttt 1800

cccagatgtg ccaatctttg gaagttgacc caatgacggc agcgaaggtt atagtcgcgg 1860

tcatgagcaa tgagagcggt ctgactctca catttgaacg acctactgag gcgaatgttg 1920

cgctagcttt acaggatcaa gagaaggctt cagaaggtgc tttggtagtt acctcaagag 1980

aagttgaaga accgtccatg aagggttcga tggccagagg agagttacaa ttagctggtc 2040

ttgctggaga tcatccggag tcgtcctatt ctaagaacga ggagatagag tctttagagc 2100

agtttcatat ggcaacggca gattcgttaa ttcgtaagca gatgagctcg attgtgtaca 2160

cgggtccgat taaagttcag caaatgaaaa actttatcga tagcctggta gcatcactat 2220

ctgctgcggt gtcgaatctc gtcaagatcc tcaaagatac agctgctatt gaccttgaaa 2280

cccgtcaaaa gtttggagtc ttggatgttg catctaggaa gtggttaatc aaaccaacgg 2340

ccaagagtca tgcatggggt gttgttgaaa cccacgcgag gaagtatcat gtggcgcttt 2400

tggaatatga tgagcagggt gtggtgacat gcgatgattg gagaagagta gctgtcagct 2460

ctgagtctgt tgtttattcc gacatggcga aactcagaac tctgcgcaga ctgcttcgaa 2520

acggagaacc gcatgtcagt agcgcaaagg ttgttcttgt ggacggagtt ccgggctgtg 2580

ggaaaaccaa agaaattctt tccagggtta attttgatga agatctaatt ttagtacctg 2640

ggaagcaagc cgcggaaatg atcagaagac gtgcgaattc ctcagggatt attgtggcca 2700

cgaaggacaa cgttaaaacc gttgattctt tcatgatgaa ttttgggaaa agcacacgct 2760

gtcagttcaa gaggttattc attgatgaag ggttgatgtt gcatactggt tgtgttaatt 2820

ttcttgtggc gatgtcattg tgcgaaattg catatgttta cggagacaca cagcagattc 2880

```
catacatcaa tagagtttca ggattcccgt accccgccca ttttgccaaa ttggaagttg    2940
acgaggtgga gacacgcaga actactctcc gttgtccagc cgatgtcaca cattatctga    3000
acaggagata tgagggcttt gtcatgagca cttcttcggt taaaaagtct gtttcgcagg    3060
agatggtcgg cggagccgcc gtgatcaatc cgatctcaaa acccttgcat ggcaagatcc    3120
tgacttttac ccaatcggat aaagaagctc tgctttcaag agggtattca gatgttcaca    3180
ctgtgcatga agtgcaaggc gagacatact ctgatgtttc actagttagg ttaaccccta    3240
caccagtctc catcattgca ggagacagcc cacatgtttt ggtcgcattg tcaaggcaca    3300
cctgttcgct caagtactac actgttgtta tggatccttt agttagtatc attagagatc    3360
tagagaaact tagctcgtac ttgttagata tgtataaggt cgatgcagga acacaatagc    3420
aattacagat tgactcggtg ttcaaaggtt ccaatctttt tgttgcagcg ccaaagactg    3480
gtgatatttc tgatatgcag ttttactatg ataagtgtct cccaggcaac agcaccatga    3540
tgaataattt tgatgctgtt accatgaggt tgactgacat ttcattgaat gtcaaagatt    3600
gcatattgga tatgtctaag tctgttgctg cgcctaagga tcaaatcaaa ccactaatac    3660
ctatggtacg aacggcggca gaaatgccac gccagactgg actattggaa aatttagtgg    3720
cgatgattaa aaggaacttt aacgcacccg agttgtctgg catcattgat attgaaaata    3780
ctgcatcttt agttgtagat aagtttttg atagttattt gcttaaagaa aaaagaaaac    3840
caaataaaaa tgtttctttg ttcagtagag agtctctcaa tagatggtta gaaaagcagg    3900
aacaggtaac aataggccag ctcgcagatt ttgattttgt agatttgcca gcagttgatc    3960
agtacagaca catgattaaa gcacaaccca agcaaaaatt ggacacttca atccaaacgg    4020
agtacccggc tttgcagacg attgtgtacc attcaaaaaa gatcaatgca atatttggcc    4080
cgttgtttag tgagcttact aggcaattac tggacagtgt tgattcgagc agatttttgt    4140
ttttcacaag aaagacacca gcgcagattg aggatttctt cggagatctc gacagtcatg    4200
tgccgatgga tgtcttggag ctggatatat caaaatacga caaatctcag aatgaattcc    4260
actgtgcagt agaatacgag atctggcgaa gattgggttt tgaagacttc ttgggagaag    4320
tttggaaaca agggcataga aagaccaccc tcaaggatta taccgcaggt ataaaaactt    4380
gcatctggta tcaaagaaag agcggggacg tcacgacgtt cattggaaac actgtgatca    4440
ttgctgcatg tttggcctcg atgcttccga tggagaaaat aatcaaagga gccttttgcg    4500
gtgacgatag tctgctgtac tttccaaagg gttgtgagtt tccggatgtg caacactccg    4560
cgaatcttat gtggaatttt gaagcaaaac tgtttaaaaa acagtatgga tacttttgcg    4620
gaagatatgt aatacatcac gacagaggat gcattgtgta ttacgatccc ctaaagttga    4680
tctcgaaact tggtgctaaa cacatcaagg attgggaaca cttggaggag ttcagaaggt    4740
```

```
ctctttgtga tgttgctgtt tcgttgaaca attgtgcgta ttacacacag ttggacgacg    4800
ctgtatggga ggttcataag accgcccctc caggttcgtt tgtttataaa agtctggtga    4860
agtatttgtc tgataaagtt ctttttagaa gtttgtttat agatggctct agttgttaaa    4920
ggaaaagtga atatcaatga gtttatcgac ctgacaaaaa tggagaagat cttaccgtcg    4980
atgtttaccc ctgtaaagag tgttatgtgt tccaaagttg ataaaataat ggttcatgag    5040
aatgagtcat tgtcagaggt gaaccttctt aaaggagtta agcttattga tagtggatac    5100
gtctgtttag ccggtttggt cgtcacgggc gagtggaact tgcctgacaa ttgcagagga    5160
ggtgtgagcg tgtgtctggt ggacaaaagg atggaaagag ccgacgaggc cactctcgga    5220
tcttactaca cagcagctgc aaagaaaaga tttcagttca aggtcgttcc caattatgct    5280
ataaccaccc aggacgcgat gaaaaacgtc tggcaagttt tagttaatat tagaaatgtg    5340
aagatgtcag cgggtttctg tccgctttct ctggagtttg tgtcggtgtg tattgtttat    5400
agaaataata taaaattagg tttgagagag aagattacaa acgtgagaga cggagggccc    5460
atggaactta cagaagaagt cgttgatgag ttcatggaag atgtccctat gtcgatcagg    5520
cttgcaaagt ttcgatctcg aaccggaaaa aagagtgatg tccgcaaagg gaaaaatagt    5580
agtaatgatc ggtcagtgcc gaacaagaac tatagaaatg ttaaggattt tggaggaatg    5640
agttttaaaa agaataattt aatcgatgat gattcggagg ctactgtcgc cgaatcggat    5700
tcgttttaaa tagatcttac agtatcacta ctccatctca gttcgtgttc ttgtcattaa    5760
ttaacaatgc aggtgctgaa caccatggtg aacaaacact tcttgtccct ttcggtcctc    5820
atcgtcctcc ttggcctctc ctccaacttg acagccggca tgcttgatat cgtgatgacc    5880
cagtctcaca aattcatgtc cacatcagta ggagacaggg tcagcatcac ctgcaaggcc    5940
agtcaggatg tgaatactgc tgtagcctgg tatcaacaga aaccaggaca ttctccgaaa    6000
ctactgattt actcggcatc cttccggtac actggagtcc ctgatcgctt cactggcaat    6060
agatctggga cggatttcac tttcaccatc agcagtgtgc aggctgaaga cctggcagtt    6120
tattactgtc agcaacatta tactactcct cccacgttcg gaggggggac caagctggag    6180
ataaaacggg ctgatgctgc accaactgta tccatcttcc caccatccag tgagcagtta    6240
acatctggag gtgcctcagt cgtgtgcttc ttgaacaact tctaccccaa agacatcaat    6300
gtcaagtgga agattgatgg cagtgaacga caaaatggcg tcctgaacag ttggactgat    6360
caggacagca aagacagcac ctacagcatg agcagcaccc tcacgttgac caaggacgag    6420
tatgaacgac ataacagcta tacctgtgag gccactcaca agacatcaac ttcacccatt    6480
gtcaagagct tcaacaggaa tgagtgtgga ggtaaacgta cgatacagga ttctgcaact    6540
gatacagttg acttaggtgc agagttgcat agagatgacc ctccacctac tgcttctgat    6600
atcggaaagc gaggcaagag gggaggtcag gttcagctgc agcagtctgg gccagagctt    6660
```

```
gtgaagccag gggcctcact caagttgtcc tgtacagctt ctggcttcaa cattaaagac   6720
acctatatac actgggtgaa acagaggcct gaacagggcc tggaatggat tggaaggatt   6780
tatcctacga atggttatac tagatatgac ccgaagttcc aggacaaggc cactataaca   6840
gcagacacat cctccaacac agcctacctg caggtcagcc gcctgacatc tgaggacact   6900
gccgtctatt attgttctag atggggaggg gacggcttct atgctatgga ctactggggt   6960
caaggagcct cagtcaccgt ctcctcagcc aaaacgacac ccccatctgt ctatccactg   7020
gcccctggat ctgctgccca aactaactcc atggtgaccc tgggatgcct ggtcaagggc   7080
tatttccctg agccagtgac agtgacctgg aactctggat ccctgtccag cggtgtgcac   7140
accttcccag ctgtcctgca gtctgacctc tacactctga gcagctcagt gactgtcccc   7200
tccagcacct ggcccagcga gaccgtcacc tgcaacgttg cccacccggc cagcagcacc   7260
aaggtggaca agaaaattgt gcccagggat tgtggttgac ctaggctcga ggggtagtca   7320
agatgcataa taaataacgg attgtgtccg taatcacacg tggtgcgtac gataacgcat   7380
agtgtttttc cctccactta aatcgaaggg ttgtgtcttg gatcgcgcgg gtcaaatgta   7440
tatggttcat atacatccgc aggcacgtaa taaagcgagg ggttcgggtc gaggtcggct   7500
gtgaaactcg aaaaggttcc ggaaaacaaa aaagagatgg taggtaatag tgttaataat   7560
aagaaaataa ataatagtgg taagaaaggt ttgaaagttg aggaaattga ggataatgta   7620
agtgatgacg agtctatcgc gtcatcgagt acgttttaat caatatgcct tatacaatca   7680
actctccgag ccaatttgtt tacttaagtt ccgcttatgc agatcctgtg cagctgatca   7740
atctgtgtac aaatgcattg ggtaaccagt ttcaaacgca acaagctagg acaacagtcc   7800
aacagcaatt tgcggatgcc tggaaacctg tgcctagtat gacagtgaga tttcctgcat   7860
cggatttcta tgtgtataga tataattcga cgcttgatcc gttgatcacg gcgttattaa   7920
atagcttcga tactagaaat agaataatag aggttgataa tcaacccgca ccgaatacta   7980
ctgaaatcgt taacgcgact cagagggtag acgatgcgac tgtagctata agggcttcaa   8040
tcaataattt ggctaatgaa ctggttcgtg gaactggcat gttcaatcaa gcaagctttg   8100
agactgctag tggacttgtc tggaccacaa ctccggctac ttagctattg ttgtgagatt   8160
tcctaaaata aagtcactga agacttaaaa ttcagggtgg ctgataccaa aatcagcagt   8220
ggttgttcgt ccacttaaat ataacgattg tcatatctgg atccaacagt taaaccatgt   8280
gatggtgtat actgtggtat ggcgtaaaac aacggaaaag tcgctgaaga cttaaaattc   8340
agggtggctg ataccaaaat cagcagtggt tgttcgtcca cttaaaaata acgattgtca   8400
tatctggatc caacagttaa accatgtgat ggtgtatact gtggtatggc gtaaaacaac   8460
ggagaggttc gaatcctccc ctaaccgcgg gtagcggccc aggtacccgg tgtgttttcc   8520
```

```
gggctgatga gtccgtgagg acgaaacctg gctgcaggca agcttggcgt aatcatggtc   8580
atagctgttt cctgtgtgaa attgttatcc gctcacaatt ccacacaaca tacgagccgg   8640
aagcataaag tgtaaagcct ggggtgccta atgagtgagc taactcacat taattgcgtt   8700
gcgctcactg cccgctttcc agtcgggaaa cctgtcgtgc cagctgcatt aatgaatcgg   8760
ccaacgcgcg gggagaggcg gtttgcgtat tgggcgctct tccgcttcct cgctcactga   8820
ctcgctgcgc tcggtcgttc ggctgcggcg agcggtatca gctcactcaa aggcggtaat   8880
acggttatcc acagaatcag gggataacgc aggaaagaac atgtgagcaa aaggccagca   8940
aaaggccagg aaccgtaaaa aggccgcgtt gctggcgttt ttccataggc tccgcccccc   9000
tgacgagcat cacaaaaatc gacgctcaag tcagaggtgg cgaaacccga caggactata   9060
aagataccag gcgtttcccc ctggaagctc cctcgtgcgc tctcctgttc cgaccctgcc   9120
gcttaccgga tacctgtccg cctttctccc ttcgggaagc gtggcgcttt ctcatagctc   9180
acgctgtagg tatctcagtt cggtgtaggt cgttcgctcc aagctgggct gtgtgcacga   9240
accccccgtt cagcccgacc gctgcgcctt atccggtaac tatcgtcttg agtccaaccc   9300
ggtaagacac gacttatcgc cactggcagc agccactggt aacaggatta gcagagcgag   9360
gtatgtaggc ggtgctacag agttcttgaa gtggtggcct aactacggct acactagaag   9420
gacagtattt ggtatctgcg ctctgctgaa gccagttacc ttcggaaaaa gagttggtag   9480
ctcttgatcc ggcaaacaaa ccaccgctgg tagcggtggt ttttttgttt gcaagcagca   9540
gattacgcgc agaaaaaaag gatctcaaga agatcctttg atcttttcta cggggtctga   9600
cgctcagtgg aacgaaaact cacgttaagg gattttggtc atgagattat caaaaaggat   9660
cttcacctag atccttttaa attaaaaatg aagttttaaa tcaatctaaa gtatatatga   9720
gtaaacttgg tctgacagtt accaatgctt aatcagtgag gcacctatct cagcgatctg   9780
tctatttcgt tcatccatag ttgcctgact ccccgtcgtg tagataacta cgatacggga   9840
gggcttacca tctggcccca gtgctgcaat gataccgcga gacccacgct caccggctcc   9900
agatttatca gcaataaacc agccagccgg aagggccgag cgcagaagtg gtcctgcaac   9960
tttatccgcc tccatccagt ctattaattg ttgccgggaa gctagagtaa gtagttcgcc  10020
agttaatagt ttgcgcaacg ttgttgccat tgctacaggc atcgtggtgt cacgctcgtc  10080
gtttggtatg gcttcattca gctccggttc ccaacgatca aggcgagtta catgatcccc  10140
catgttgtgc aaaaaagcgg ttagctcctt cggtcctccg atcgttgtca gaagtaagtt  10200
ggccgcagtg ttatcactca tggttatggc agcactgcat aattctctta ctgtcatgcc  10260
atccgtaaga tgcttttctg tgactggtga gtactcaacc aagtcattct gagaatagtg  10320
tatgcggcga ccgagttgct cttgcccggc gtcaatacgg gataataccg cgccacatag  10380
cagaacttta aaagtgctca tcattggaaa acgttcttcg gggcgaaaac tctcaaggat  10440
```

```
cttaccgctg ttgagatcca gttcgatgta acccactcgt gcacccaact gatcttcagc   10500
atcttttact ttcaccagcg tttctgggtg agcaaaaaca ggaaggcaaa atgccgcaaa   10560
aaagggaata agggcgacac ggaaatgttg aatactcata ctcttccttt ttcaatatta   10620
ttgaagcatt tatcagggtt attgtctcat gagcggatac atatttgaat gtatttagaa   10680
aaataaacaa ataggggttc cgcgcacatt tccccgaaaa gtgccacctg acgtctaaga   10740
aaccattatt atcatgacat taacctataa aaataggcgt atcacgaggc cctttcgtct   10800
cgcgcgtttc ggtgatgacg gtgaaaacct ctgacacatg cagctcccgg agacggtcac   10860
agcttgtctg taagcggatg ccgggagcag acaagcccgt cagggcgcgt cagcgggtgt   10920
tggcgggtgt cggggctggc ttaactatgc ggcatcagag cagattgtac tgagagtgca   10980
ccatatgcgg tgtgaaatac cgcacagatg cgtaaggaga aaataccgca tcaggcgcca   11040
ttcgccattc aggctgcgca actgttggga agggcgatcg gtgcgggcct cttcgctatt   11100
acgccagctg gcgaaagggg gatgtgctgc aaggcgatta agttgggtaa cgccagggtt   11160
ttcccagtca cgacgttgta aaacgacggc cagtgaattc aagcttaata cgactcacta   11220
ta                                                                  11222
```

```
<210>  74
<211>  510
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  pLSBC1741 , see Example 13

<400>  74

Met Gln Val Leu Asn Thr Met Val Asn Lys His Phe Leu Ser Leu Ser
1               5                   10                  15


Val Leu Ile Val Leu Leu Gly Leu Ser Ser Asn Leu Thr Ala Gly Met
            20                  25                  30


Leu Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val
        35                  40                  45


Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Asn Thr
    50                  55                  60


Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly His Ser Pro Lys Leu Leu
65                  70                  75                  80


Ile Tyr Ser Ala Ser Phe Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr
                85                  90                  95
```

```
Gly Asn Arg Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln
            100                 105                 110

Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro
        115                 120                 125

Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala
    130                 135                 140

Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser
145                 150                 155                 160

Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp
                165                 170                 175

Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val
            180                 185                 190

Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met
        195                 200                 205

Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser
    210                 215                 220

Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys
225                 230                 235                 240

Ser Phe Asn Arg Asn Glu Cys Gly Gly Lys Arg Thr Ile Gln Asp Ser
                245                 250                 255

Ala Thr Asp Thr Val Asp Leu Gly Ala Glu Leu His Arg Asp Asp Pro
            260                 265                 270

Pro Pro Thr Ala Ser Asp Ile Gly Lys Arg Gly Lys Arg Gly Gly Gln
        275                 280                 285

Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
    290                 295                 300

Leu Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
305                 310                 315                 320

Ile His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
                325                 330                 335

Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Asp Pro Lys Phe Gln
            340                 345                 350
```

```
Asp Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr Leu
        355                 360                 365

Gln Val Ser Arg Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ser
    370                 375                 380

Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln Gly
385                 390                 395                 400

Ala Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
                405                 410                 415

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
            420                 425                 430

Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp
        435                 440                 445

Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu
    450                 455                 460

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser
465                 470                 475                 480

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
                485                 490                 495

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly
            500                 505                 510


<210>  75
<211>  120
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  pLSBC1731 , see Example 15

<400>  75
ggaggtaaac gtacgataca ggattctgca actgatacag ttgacttagg tgcagagttg      60

catagagatg accctccacc tactgcttct gatatcggaa agcgaggcaa gaggggaggt     120


<210>  76
<211>  40
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  pLSBC1731 , see Example 15
```

```
<400>  76

Gly Gly Lys Arg Thr Ile Gln Asp Ser Ala Thr Asp Thr Val Asp Leu
1               5                   10                  15


Gly Ala Glu Leu His Arg Asp Asp Pro Pro Pro Thr Ala Ser Asp Ile
            20                  25                  30


Gly Lys Arg Gly Lys Arg Gly Gly
        35                  40


<210>  77
<211>  1353
<212>  DNA
<213>  Murine [p9E10Hy-TOPO, see Example 3]

<400>  77
gaagtagatc tggttgagtc tgggggagac ttagtgaagc ctggagggtc cctgaaactc      60

tcctgtgcag cctctggatt cactttcagt cactatggca tgtcttgggt tcgccagact     120

ccagacaaga ggctggagtg ggtcgcaacc attggtagtc gtggtactta cacccactat     180

ccagacagtg tgaagggacg attcaccatc tccagagaca atgacaagaa cgccctgtac     240

ctgcaaatga acagtctgaa gtctgaagac acagccatgt attactgtgc aagaagaagt     300

gaattttatt actacggtaa tacctactat tactctgcta tggactactg gggtcaagga     360

gcctcagtca ccgtctcctc agccaaaacg acacccccat ctgtctatcc actggcccct     420

ggatctgctg cccaaactaa ctccatggtg accctgggat gcctggtcaa gggctatttc     480

cctgagccag tgacagtgac ctggaactct ggatccctgt ccagcggtgt gcacaccttc     540

ccagctgtcc tgcagtctga cctccacact ctgagcagct cagtgactgt cccctccagc     600

acctggccca gcgagaccgt cacctgcaac gttgcccacc cggccagcag caccaaggtg     660

gacaagaaaa ttgtgcccag ggattgtggt tgtaagcctt gcatatgtac agtcccagaa     720

gtatcatctg tcttcatctt ccccccaaag cccaaggatg tgctcaccat tactctgact     780

cctaaggtca cgtgtgttgt ggtagacatc agcaaggatg atcccgaggt ccagttcagc     840

tggtttgtag atgatgtgga ggtgcacaca gctcagacgc aaccccggga ggagcagttc     900

aacagcactt tccgctcagt cagtgaactt cccatcatgc accaggactg gctcaatgac     960

aaggagttca aatgcagggt caacagtgca gctttccctg cccccatcga gaaaaccatc    1020

tccaaaacca aaggcagacc gaaggctcca caggtgtaca ccattccacc tcccaaggag    1080

cagatggcca aggataaagt cagtctgacc tgcatgataa cagacttctt ccctgaagac    1140

attactgtgg agtggcagtg gaatgggcag ccagcggaga actacaagaa cactcagccc    1200

atcatggaca cagatggctc ttacttcgtc tacagcaagc tcaatgtgca gaagagcaac    1260
```

```
tgggaggcag gaaatacttt cacctgctct gtgttacatg agggcctgca caaccaccat   1320

actgagaaga gcctctccca ctctcctggt aaa                                1353


<210>  78
<211>  451
<212>  PRT
<213>  Murine [p9E10Hy-TOPO, see Example 3]

<400>  78

Glu Val Asp Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr
            20                  25                  30


Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Trp Val
        35                  40                  45


Ala Thr Ile Gly Ser Arg Gly Thr Tyr Thr His Tyr Pro Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Asp Lys Asn Ala Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95


Ala Arg Arg Ser Glu Phe Tyr Tyr Tyr Gly Asn Thr Tyr Tyr Tyr Ser
            100                 105                 110


Ala Met Asp Tyr Trp Gly Gln Gly Ala Ser Val Thr Val Ser Ser Ala
        115                 120                 125


Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala
    130                 135                 140


Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe
145                 150                 155                 160


Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
                165                 170                 175


Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu His Thr Leu Ser
            180                 185                 190


Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
        195                 200                 205
```

```
Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
    210                 215                 220


Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
225                 230                 235                 240


Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
                245                 250                 255


Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
            260                 265                 270


Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
        275                 280                 285


His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
    290                 295                 300


Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Asp
305                 310                 315                 320


Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
                325                 330                 335


Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
            340                 345                 350


Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
        355                 360                 365


Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
    370                 375                 380


Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
385                 390                 395                 400


Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val
                405                 410                 415


Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
            420                 425                 430


His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
        435                 440                 445


Pro Gly Lys
    450
```

```
<210>  79
<211>  654
<212>  DNA
<213>  Murine [p9E10Lt-TOPO see Example 3]

<400>  79
gacattgtgc tgacccaatc tccagcttct ttggctgtat ctctaggaca gagggccacc      60

atctcctgca gagccagcga aagtgttgat aattatggct ttagttttat gaactggttc     120

caacagaaac caggacagcc acccaaactc ctcatctatg ctatatccaa ccgaggatcc     180

ggggtccctg ccaggtttag tggcagtggg tctgggacag acttcagcct caacatccat     240

cctgtagagg aggatgatcc tgcaatgtat ttctgtcagc aaactaagga ggttccgtgg     300

acgttcggtg gaggcaccaa gctggaaatc aaacgggctg atgctgcacc aactgtatcc     360

atcttcccac catccagtga gcagttaaca tctggaggtg cctcagtcgt gtgcttcttg     420

aacaacttct accccaaaga catcaatgtc aagtggaaga ttgatggcag tgaacgacaa     480

aatggcgtcc tgaacagttg gactgatcag gacagcaaag acagcaccta cagcatgagc     540

agcaccctca cgttgaccaa ggacgagtat gaacgacata acagctatac ctgtgaggcc     600

actcacaaga catcaacttc acccattgtc aagagcttca acaggaatga gtgt           654


<210>  80
<211>  218
<212>  PRT
<213>  Murine [p9E10Lt-TOPO, see Example 3]

<400>  80

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Asn Tyr
            20                  25                  30


Gly Phe Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45


Lys Leu Leu Ile Tyr Ala Ile Ser Asn Arg Gly Ser Gly Val Pro Ala
    50                  55                  60


Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His
65                  70                  75                  80


Pro Val Glu Glu Asp Asp Pro Ala Met Tyr Phe Cys Gln Gln Thr Lys
                85                  90                  95


Glu Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
```

100 105 110

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
115 120 125

Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
130 135 140

Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
145 150 155 160

Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
180 185 190

His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
195 200 205

Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
210 215

<210> 81
<211> 666
<212> DNA
<213> Artificial Sequence

<220>
<223> p4D5Hy-TOPO, see Example 11

<400> 81
caggttcagc tgcagcagtc tgggccagag cttgtgaagc caggggcctc actcaagttg 60

tcctgtacag cttctggctt caacattaaa gacacctata tacactgggt gaaacagagg 120

cctgaacagg gcctggaatg gattggaagg atttatccta cgaatggtta tactagatat 180

gacccgaagt tccaggacaa ggccactata acagcagaca catcctccaa cacagcctac 240

ctgcaggtca gccgcctgac atctgaggac actgccgtct attattgttc tagatgggga 300

ggggacggct tctatgctat ggactactgg ggtcaaggag cctcagtcac cgtctcctca 360

gccaaaacga cacccccatc tgtctatcca ctggcccctg grtctgctgc ccaaactaac 420

tccatggtga ccctgggatg cctggtcaag ggctatttcc ctgagccagt gacagtgacc 480

tggaactctg gatccctgtc cagcggtgtg cacaccttcc cagctgtcct gcagtctgac 540

ctctacactc tgagcagctc agtgactgtc ccctccagca cctggcccag cgagaccgtc 600

acctgcaacg ttgcccaccc ggccagcagc accaaggtgg acaagaaaat tgtgcccagg 660

gattgt 666

```
<210>  82
<211>  222
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  p4D5Hy-TOPO, see Exampl 11

<400>  82

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15


Ser Leu Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
            20                  25                  30


Tyr Ile His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Asp Pro Lys Phe
    50                  55                  60


Gln Asp Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65                  70                  75                  80


Leu Gln Val Ser Arg Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Ala Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
        115                 120                 125


Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
    130                 135                 140


Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
145                 150                 155                 160


Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175


Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
            180                 185                 190


Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala
        195                 200                 205
```

```
Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys
    210                 215                 220


<210>  83
<211>  642
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  p4D5Lt-TOPO, see Example 11

<400>  83
gatatcgtga tgacccagtc tcacaaattc atgtccacat cagtaggaga cagggtcagc      60

atcacctgca aggccagtca ggatgtgaat actgctgtag cctggtatca acagaaacca     120

ggacattctc cgaaactact gatttactcg gcatccttcc ggtacactgg agtccctgat     180

cgcttcactg gcaatagatc tgggacggat ttcactttca ccatcagcag tgtgcaggct     240

gaagacctgg cagtttatta ctgtcagcaa cattatacta ctcctcccac gttcggaggg     300

gggaccaagc tggagataaa acgggctgat gctgcaccaa ctgtatccat cttcccacca     360

tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gcttcttgaa caacttctac     420

cccaaagaca tcaatgtcaa gtggaagatt gatggcagtg aacgacaaaa tggcgtcctg     480

aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcacg     540

ttgaccaagg acgagtatga acgacataac agctatacct gtgaggccac tcacaagaca     600

tcaacttcac ccattgtcaa gagcttcaac aggaatgagt gt                        642


<210>  84
<211>  214
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  p4D5Lt-TOPO, see Example 11

<400>  84

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
1               5                   10                  15


Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Asn Thr Ala
            20                  25                  30


Val Ala Trp Tyr Gln Gln Lys Pro Gly His Ser Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ser Ala Ser Phe Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60
```

```
Asn Arg Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Ala
65                  70                  75                  80

Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala
            100                 105                 110

Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly
        115                 120                 125

Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile
    130                 135                 140

Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
145                 150                 155                 160

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
                165                 170                 175

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
            180                 185                 190

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
        195                 200                 205

Phe Asn Arg Asn Glu Cys
    210


<210>  85
<211>  1671
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  pLSBC1736, see Example 15

<400>  85
gcatgcatgc aggtgctgaa caccatggtg aacaaacact tcttgtccct ttcggtcctc      60

atcgtcctcc ttggcctctc ctccaacttg acagccggca tgcaggtgct gaacaccatg     120

gtgaacaaac acttcttgtc cctttcggtc ctcatcgtcc tccttggcct ctcctccaac     180

ttgacagccg gcatgctaga agtagatctg gttgagtctg gggagactt agtgaagcct      240

ggagggtccc tgaaactctc ctgtgcagcc tctggattca ctttcagtca ctatggcatg     300

tcttgggttc gccagactcc agacaagagg ctggagtggg tcgcaaccat tggtagtcgt     360

ggtacttaca cccactatcc agacagtgtg aagggacgat tcaccatctc cagagacaat     420
```

gacaagaacg ccctgtacct gcaaatgaac agtctgaagt ctgaagacac agccatgtat 480

tactgtgcaa gaagaagtga attttattac tacggtaata cctactatta ctctgctatg 540

gactactggg gtcaaggagc ctcagtcacc gtctcctcag ccaaaacgac acccccatct 600

gtctatccac tggcccctgg atctgctgcc caaactaact ccatggtgac cctgggatgc 660

ctggtcaagg gctatttccc tgagccagtg acagtgacct ggaactctgg atccctgtcc 720

agcggtgtgc acaccttccc agctgtcctg cagtctgacc tccacactct gagcagctca 780

gtgactgtcc cctccagcac ctggcccagc gagaccgtca cctgcaacgt tgcccacccg 840

gccagcagca ccaaggtgga caagaaaatt gtgcccaggg attgtggcgg aggtaaacgt 900

acgatacagg attctgcaac tgatacagtt gacttaggtg cagagttgca tagagatgac 960

cctccaccta ctgcttctga tatcggaaag cgaggcaaga ggggaggtga cattgtgctg 1020

acccaatctc cagcttcttt ggctgtatct ctaggacaga gggccaccat ctcctgcaga 1080

gccagcgaaa gtgttgataa ttatggcttt agttttatga actggttcca acagaaacca 1140

ggacagccac ccaaactcct catctatgct atatccaacc gaggatccgg ggtccctgcc 1200

aggtttagtg gcagtgggtc tgggacagac ttcagcctca acatccatcc tgtagaggag 1260

gatgatcctg caatgtattt ctgtcagcaa actaaggagg ttccgtggac gttcggtgga 1320

ggcaccaagc tggaaatcaa acgggctgat gctgcaccaa ctgtatccat cttcccacca 1380

tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gcttcttgaa caacttctac 1440

cccaaagaca tcaatgtcaa gtggaagatt gatggcagtg aacgacaaaa tggcgtcctg 1500

aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcacg 1560

ttgaccaagg acgagtatga acgacataac agctatacct gtgaggccac tcacaagaca 1620

tcaacttcac ccattgtcaa gagcttcaac aggaatgagt gttagcctag g 1671

<210> 86
<211> 552
<212> PRT
<213> Artificial Sequence

<220>
<223> pLSBC1736, see Example 15

<400> 86

Met Gln Val Leu Asn Thr Met Val Asn Lys His Phe Leu Ser Leu Ser
1 5 10 15

Val Leu Ile Val Leu Leu Gly Leu Ser Ser Asn Leu Thr Ala Gly Met
20 25 30

Gln Val Leu Asn Thr Met Val Asn Lys His Phe Leu Ser Leu Ser Val
35 40 45

```
Leu Ile Val Leu Leu Gly Leu Ser Ser Asn Leu Thr Ala Gly Met Leu
    50                  55                  60

Glu Val Asp Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
65                  70                  75                  80

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr
                85                  90                  95

Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Trp Val
            100                 105                 110

Ala Thr Ile Gly Ser Arg Gly Thr Tyr Thr His Tyr Pro Asp Ser Val
        115                 120                 125

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Asp Lys Asn Ala Leu Tyr
    130                 135                 140

Leu Gln Met Asn Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
145                 150                 155                 160

Ala Arg Arg Ser Glu Phe Tyr Tyr Tyr Gly Asn Thr Tyr Tyr Tyr Ser
                165                 170                 175

Ala Met Asp Tyr Trp Gly Gln Gly Ala Ser Val Thr Val Ser Ser Ala
            180                 185                 190

Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala
        195                 200                 205

Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe
    210                 215                 220

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
225                 230                 235                 240

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu His Thr Leu Ser
                245                 250                 255

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
            260                 265                 270

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
        275                 280                 285

Val Pro Arg Asp Cys Gly Gly Gly Lys Arg Thr Ile Gln Asp Ser Ala
```

```
    290                 295                 300

Thr Asp Thr Val Asp Leu Gly Ala Glu Leu His Arg Asp Asp Pro Pro
305                 310                 315                 320

Pro Thr Ala Ser Asp Ile Gly Lys Arg Gly Lys Arg Gly Gly Asp Ile
                325                 330                 335

Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg
            340                 345                 350

Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Asn Tyr Gly Phe
        355                 360                 365

Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu
    370                 375                 380

Leu Ile Tyr Ala Ile Ser Asn Arg Gly Ser Gly Val Pro Ala Arg Phe
385                 390                 395                 400

Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His Pro Val
                405                 410                 415

Glu Glu Asp Asp Pro Ala Met Tyr Phe Cys Gln Gln Thr Lys Glu Val
            420                 425                 430

Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp
        435                 440                 445

Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr
    450                 455                 460

Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys
465                 470                 475                 480

Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly
                485                 490                 495

Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser
            500                 505                 510

Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn
        515                 520                 525

Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val
    530                 535                 540
```

```
Lys Ser Phe Asn Arg Asn Glu Cys
545                 550


<210>  87
<211>  1526
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  HufAb H2, see Example 2


<220>
<221>  misc_feature
<222>  (704)..(704)
<223>  n is a, c, g, or t

<400>  87
ttaattaaca tggacatgag ggtccccgct cagctcctgg ggctcctgct gctctggctc      60

tcaggtgcca gatgtgacat ccagatgacc cagtctccat cctccctgtc tgcatctgta     120

ggagacagag tcaccatcac ttgccaggcg agtcaggaca ttagcaacta tttaaattgg     180

tatcaccaga aaccagggaa agcccctgag ctcctgatct acgatgcatc caatttggaa     240

acaggggtcc catcaaggtt cagtggaagt ggatatggga cagattttac tttaactatc     300

agcagcctgc agcctgaaga ttttgcaaca tattactgtc aacagtatga taatctcccg     360

ctcactttcg gcggagggac caaggtggag atcaaacgaa ctgtggctgc accatctgtc     420

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg     480

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa     540

tcgggtaact cccaggagag tgtcacagag caggacagca aggacggcac ctacagcctc     600

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa     660

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcancagggg agagtgtgga     720

ggtaaacgta cgatacagga ttctgcaact gatacagttg acttaggtgc agagttgcat     780

agagatgacc ctccacctac tgcttctgat atcggaaagc gaggcaagag gggaggtgag     840

gtgcagctgg tggagtctgg gggaggcttg gtccagcctg gggggtccct gagactctct     900

tgtgcagcct ctggattcac atttagaaac tattacatgg gctgggtccg ccaggctcct     960

gggaaggggc tagagtgggt ggccaatgtt aagcaagatg gatctgaaca atactatacg    1020

gactctgtga ggggccgctt caccttctcc agagacaacg ccaagaactc gctgtatcta    1080

caaatgaaca gcctcagagt cgacgacacg gctatgtatt actgtgcgag ggggcgtagt    1140

tgggatgctt ttgataagtg gggccaaggg acaatggtca ccgtctcttc agcctccacc    1200

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg    1260

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca    1320
```

```
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac   1380

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc   1440

aacgtgaatc acaagcccag caacaccaag gtggacaaga gagttgagcc caaatcttgt   1500

gacaaaactc acacatgagc ggccgc                                        1526


<210>  88
<211>  502
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HufAb H2 , see Example 2


<220>
<221>  misc_feature
<222>  (232)..(232)
<223>  Xaa can be any naturally occurring amino acid

<400>  88

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1               5                   10                  15


Leu Ser Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
            20                  25                  30


Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser
        35                  40                  45


Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr His Gln Lys Pro Gly Lys
    50                  55                  60


Ala Pro Glu Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val
65                  70                  75                  80


Pro Ser Arg Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Leu Thr
                85                  90                  95


Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
            100                 105                 110


Tyr Asp Asn Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
        115                 120                 125


Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
    130                 135                 140


Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145                 150                 155                 160
```

```
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
                165                 170                 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
            180                 185                 190

Gly Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
        195                 200                 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
    210                 215                 220

Ser Pro Val Thr Lys Ser Phe Xaa Arg Gly Glu Cys Gly Gly Lys Arg
225                 230                 235                 240

Thr Ile Gln Asp Ser Ala Thr Asp Thr Val Asp Leu Gly Ala Glu Leu
                245                 250                 255

His Arg Asp Asp Pro Pro Pro Thr Ala Ser Asp Ile Gly Lys Arg Gly
            260                 265                 270

Lys Arg Gly Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
        275                 280                 285

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
    290                 295                 300

Phe Arg Asn Tyr Tyr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly
305                 310                 315                 320

Leu Glu Trp Val Ala Asn Val Lys Gln Asp Gly Ser Glu Gln Tyr Tyr
                325                 330                 335

Thr Asp Ser Val Arg Gly Arg Phe Thr Phe Ser Arg Asp Asn Ala Lys
            340                 345                 350

Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Val Asp Asp Thr Ala
        355                 360                 365

Met Tyr Tyr Cys Ala Arg Gly Arg Ser Trp Asp Ala Phe Asp Lys Trp
    370                 375                 380

Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
385                 390                 395                 400

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
```

```
                405                 410                 415

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
            420                 425                 430

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
        435                 440                 445

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
    450                 455                 460

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
465                 470                 475                 480

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
                485                 490                 495

Cys Asp Lys Thr His Thr
            500


<210>  89
<211>  2748
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  pLSBC1766, see Example 12

<400>  89
ttaattaaca atgcaggtgc tgaacaccat ggtgaacaaa cacttcttgt ccctttcggt      60

cctcatcgtc ctccttggcc tctcctccaa cttgacagcc ggcatgcagg ttcagctgca     120

gcagtctggg ccagagcttg tgaagccagg ggcctcactc aagttgtcct gtacagcttc     180

tggcttcaac attaaagaca cctatataca ctgggtgaaa cagaggcctg aacagggcct     240

ggaatggatt ggaaggattt atcctacgaa tggttatact agatatgacc cgaagttcca     300

ggacaaggcc actataacag cagacacatc ctccaacaca gcctacctgc aggtcagccg     360

cctgacatct gaggacactg ccgtctatta ttgttctaga tggggagggg acggcttcta     420

tgctatggac tactggggtc aaggagcctc agtcaccgtc tcctcagcca aaacgacacc     480

cccatctgtc tatccactgg cccctggrtc tgctgcccaa actaactcca tggtgaccct     540

gggatgcctg gtcaagggct atttccctga gccagtgaca gtgacctgga actctggatc     600

cctgtccagc ggtgtgcaca ccttcccagc tgtcctgcag tctgacctct acactctgag     660

cagctcagtg actgtcccct ccagcacctg gcccagcgag accgtcacct gcaacgttgc     720

ccacccggcc agcagcacca aggtggacaa gaaaattgtg cccagggatt gtggtggagg     780

taaacgtacg atacaggatt ctgcaactga tacagttgac ttaggtgcag agttgcatag     840
```

```
agatgaccct ccacctactg cttctgatat cggaaagcga ggcaagaggg gaggtgatat     900
cgtgatgacc cagtctcaca aattcatgtc cacatcagta ggagacaggg tcagcatcac     960
ctgcaaggcc agtcaggatg tgaatactgc tgtagcctgg tatcaacaga aaccaggaca    1020
ttctccgaaa ctactgattt actcggcatc cttccggtac actggagtcc ctgatcgctt    1080
cactggcaat agatctggga cggatttcac tttcaccatc agcagtgtgc aggctgaaga    1140
cctggcagtt tattactgtc agcaacatta tactactcct cccacgttcg gaggggggac    1200
caagctggag ataaaacggg ctgatgctgc accaactgta tccatcttcc caccatccag    1260
tgagcagtta acatctggag gtgcctcagt cgtgtgcttc ttgaacaact tctaccccaa    1320
agacatcaat gtcaagtgga agattgatgg cagtgaacga caaaatggcg tcctgaacag    1380
ttggactgat caggacagca aagacagcac ctacagcatg agcagcaccc tcacgttgac    1440
caaggacgag tatgaacgac ataacagcta tacctgtgag gccactcaca agacatcaac    1500
ttcacccatt gtcaagagct tcaacaggaa tgagtgttag cctaggctcg aggggtagtc    1560
aagatgcata ataaataacg gattgtgtcc gtaatcacac gtggtgcgta cgataacgca    1620
tagtgttttt ccctccactt aaatcgaagg gttgtgtctt ggatcgcgcg ggtcaaatgt    1680
atatggttca tatacatccg caggcacgta ataaagcgag gggttcgggt cgaggtcggc    1740
tgtgaaactc gaaaaggttc cggaaaacaa aaaagagatg gtaggtaata gtgttaataa    1800
taagaaaata aataatagtg gtaagaaagg tttgaaagtt gaggaaattg aggataatgt    1860
aagtgatgac gagtctatcg cgtcatcgag tacgttttaa tcaatatgcc ttatacaatc    1920
aactctccga gccaatttgt ttacttaagt tccgcttatg cagatcctgt gcagctgatc    1980
aatctgtgta caaatgcatt gggtaaccag tttcaaacgc aacaagctag gacaacagtc    2040
caacagcaat ttgcggatgc ctggaaacct gtgcctagta tgacagtgag atttcctgca    2100
tcggatttct atgtgtatag atataattcg acgcttgatc cgttgatcac ggcgttatta    2160
aatagcttcg atactagaaa tagaataata gaggttgata atcaacccgc accgaatact    2220
actgaaatcg ttaacgcgac tcagagggta gacgatgcga ctgtagctat aagggcttca    2280
atcaataatt tggctaatga actggttcgt ggaactggca tgttcaatca agcaagcttt    2340
gagactgcta gtggacttgt ctggaccaca actccggcta cttagctatt gttgtgagat    2400
ttcctaaaat aaagtcactg aagacttaaa attcagggtg gctgatacca aaatcagcag    2460
tggttgttcg tccacttaaa tataacgatt gtcatatctg gatccaacag ttaaaccatg    2520
tgatggtgta tactgtggta tggcgtaaaa caacggaaaa gtcgctgaag acttaaaatt    2580
cagggtggct gataccaaaa tcagcagtgg ttgttcgtcc acttaaaaat aacgattgtc    2640
atatctggat ccaacagtta aaccatgtga tggtgtatac tgtggtatgg cgtaaaacaa    2700
```

```
cggagaggtt cgaatcctcc cctaaccgcg ggtagcggcc caggtacc                2748


<210>  90
<211>  509
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  pLSBC1766, see Example 12

<400>  90

Met Gln Val Leu Asn Thr Met Val Asn Lys His Phe Leu Ser Leu Ser
1               5                   10                  15


Val Leu Ile Val Leu Leu Gly Leu Ser Ser Asn Leu Thr Ala Gly Met
            20                  25                  30


Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
        35                  40                  45


Ser Leu Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
    50                  55                  60


Tyr Ile His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
65                  70                  75                  80


Gly Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Asp Pro Lys Phe
                85                  90                  95


Gln Asp Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
            100                 105                 110


Leu Gln Val Ser Arg Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
        115                 120                 125


Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
    130                 135                 140


Gly Ala Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
145                 150                 155                 160


Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
                165                 170                 175


Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
            180                 185                 190


Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
        195                 200                 205
```

```
Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
    210                 215                 220

Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala
225                 230                 235                 240

Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Gly
                245                 250                 255

Gly Lys Arg Thr Ile Gln Asp Ser Ala Thr Asp Thr Val Asp Leu Gly
            260                 265                 270

Ala Glu Leu His Arg Asp Asp Pro Pro Pro Thr Ala Ser Asp Ile Gly
        275                 280                 285

Lys Arg Gly Lys Arg Gly Gly Asp Ile Val Met Thr Gln Ser His Lys
    290                 295                 300

Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala
305                 310                 315                 320

Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly
                325                 330                 335

His Ser Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Arg Tyr Thr Gly
            340                 345                 350

Val Pro Asp Arg Phe Thr Gly Asn Arg Ser Gly Thr Asp Phe Thr Phe
        355                 360                 365

Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln
    370                 375                 380

Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu
385                 390                 395                 400

Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser
                405                 410                 415

Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn
            420                 425                 430

Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser
        435                 440                 445

Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys
```

```
    450                 455                 460


Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu
465                 470                 475                 480


Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser
                485                 490                 495


Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
            500                 505


<210>  91
<211>  2751
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  PLSBC1767, see Example 13

<400>  91
ttaattaaca atgcaggtgc tgaacaccat ggtgaacaaa cacttcttgt ccctttcggt      60

cctcatcgtc ctccttggcc tctcctccaa cttgacagcc ggcatgcttg atatcgtgat     120

gacccagtct cacaaattca tgtccacatc agtaggagac agggtcagca tcacctgcaa     180

ggccagtcag gatgtgaata ctgctgtagc ctggtatcaa cagaaaccag gacattctcc     240

gaaactactg atttactcgg catccttccg gtacactgga gtccctgatc gcttcactgg     300

caatagatct gggacggatt tcactttcac catcagcagt gtgcaggctg aagacctggc     360

agtttattac tgtcagcaac attatactac tcctcccacg ttcggagggg ggaccaagct     420

ggagataaaa cgggctgatg ctgcaccaac tgtatccatc ttcccaccat ccagtgagca     480

gttaacatct ggaggtgcct cagtcgtgtg cttcttgaac aacttctacc ccaaagacat     540

caatgtcaag tggaagattg atggcagtga acgacaaaat ggcgtcctga acagttggac     600

tgatcaggac agcaaagaca gcacctacag catgagcagc accctcacgt tgaccaagga     660

cgagtatgaa cgacataaca gctatacctg tgaggccact cacaagacat caacttcacc     720

cattgtcaag agcttcaaca ggaatgagtg tggaggtaaa cgtacgatac aggattctgc     780

aactgataca gttgacttag gtgcagagtt gcatagagat gaccctccac ctactgcttc     840

tgatatcgga aagcgaggca agaggggagg tcaggttcag ctgcagcagt ctgggccaga     900

gcttgtgaag ccaggggcct cactcaagtt gtcctgtaca gcttctggct tcaacattaa     960

agacacctat atacactggg tgaaacagag gcctgaacag ggcctggaat ggattggaag    1020

gatttatcct acgaatggtt atactagata tgacccgaag ttccaggaca aggccactat    1080

aacagcagac acatcctcca acacagccta cctgcaggtc agccgcctga catctgagga    1140

cactgccgtc tattattgtt ctagatgggg aggggacggc ttctatgcta tggactactg    1200
```

```
gggtcaagga gcctcagtca ccgtctcctc agccaaaacg acacccccat ctgtctatcc   1260
actggcccct ggatctgctg cccaaactaa ctccatggtg accctgggat gcctggtcaa   1320
gggctatttc cctgagccag tgacagtgac ctggaactct ggatccctgt ccagcggtgt   1380
gcacaccttc ccagctgtcc tgcagtctga cctctacact ctgagcagct cagtgactgt   1440
cccctccagc acctggccca gcgagaccgt cacctgcaac gttgcccacc cggccagcag   1500
caccaaggtg gacaagaaaa ttgtgcccag ggattgtggt tgacctaggc tcgaggggta   1560
gtcaagatgc ataataaata acggattgtg tccgtaatca cacgtggtgc gtacgataac   1620
gcatagtgtt tttccctcca cttaaatcga agggttgtgt cttggatcgc gcgggtcaaa   1680
tgtatatggt tcatatacat ccgcaggcac gtaataaagc gaggggttcg ggtcgaggtc   1740
ggctgtgaaa ctcgaaaagg ttccggaaaa caaaaaagag atggtaggta atagtgttaa   1800
taataagaaa ataaataata gtggtaagaa aggtttgaaa gttgaggaaa ttgaggataa   1860
tgtaagtgat gacgagtcta tcgcgtcatc gagtacgttt taatcaatat gccttataca   1920
atcaactctc cgagccaatt tgtttactta agttccgctt atgcagatcc tgtgcagctg   1980
atcaatctgt gtacaaatgc attgggtaac cagtttcaaa cgcaacaagc taggacaaca   2040
gtccaacagc aatttgcgga tgcctggaaa cctgtgccta gtatgacagt gagatttcct   2100
gcatcggatt tctatgtgta tagatataat tcgacgcttg atccgttgat cacggcgtta   2160
ttaaatagct tcgatactag aaatagaata atagaggttg ataatcaacc cgcaccgaat   2220
actactgaaa tcgttaacgc gactcagagg gtagacgatg cgactgtagc tataagggct   2280
tcaatcaata atttggctaa tgaactggtt cgtggaactg gcatgttcaa tcaagcaagc   2340
tttgagactg ctagtggact tgtctggacc acaactccgg ctacttagct attgttgtga   2400
gatttcctaa aataaagtca ctgaagactt aaaattcagg gtggctgata ccaaaatcag   2460
cagtggttgt tcgtccactt aaatataacg attgtcatat ctggatccaa cagttaaacc   2520
atgtgatggt gtatactgtg gtatggcgta aaacaacgga aaagtcgctg aagacttaaa   2580
attcagggtg gctgatacca aaatcagcag tggttgttcg tccacttaaa aataacgatt   2640
gtcatatctg gatccaacag ttaaaccatg tgatggtgta tactgtggta tggcgtaaaa   2700
caacggagag gttcgaatcc tcccctaacc gcgggtagcg gcccaggtac c            2751
```

<210> 92
<211> 510
<212> PRT
<213> Artificial Sequence

<220>
<223> pLSBC1767, see Example 13

<400> 92

```
Met Gln Val Leu Asn Thr Met Val Asn Lys His Phe Leu Ser Leu Ser
1               5                   10                  15

Val Leu Ile Val Leu Leu Gly Leu Ser Ser Asn Leu Thr Ala Gly Met
            20                  25                  30

Leu Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val
        35                  40                  45

Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Asn Thr
    50                  55                  60

Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly His Ser Pro Lys Leu Leu
65                  70                  75                  80

Ile Tyr Ser Ala Ser Phe Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr
                85                  90                  95

Gly Asn Arg Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln
            100                 105                 110

Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro
        115                 120                 125

Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala
    130                 135                 140

Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser
145                 150                 155                 160

Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp
                165                 170                 175

Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val
            180                 185                 190

Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met
        195                 200                 205

Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser
    210                 215                 220

Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys
225                 230                 235                 240

Ser Phe Asn Arg Asn Glu Cys Gly Gly Lys Arg Thr Ile Gln Asp Ser
                245                 250                 255
```

```
Ala Thr Asp Thr Val Asp Leu Gly Ala Glu Leu His Arg Asp Asp Pro
            260                 265                 270

Pro Pro Thr Ala Ser Asp Ile Gly Lys Arg Gly Lys Arg Gly Gly Gln
        275                 280                 285

Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
    290                 295                 300

Leu Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
305                 310                 315                 320

Ile His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
                325                 330                 335

Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Asp Pro Lys Phe Gln
            340                 345                 350

Asp Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr Leu
        355                 360                 365

Gln Val Ser Arg Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ser
    370                 375                 380

Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln Gly
385                 390                 395                 400

Ala Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
                405                 410                 415

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
            420                 425                 430

Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp
        435                 440                 445

Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu
    450                 455                 460

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser
465                 470                 475                 480

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
                485                 490                 495

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly
```

500 505 510

<210> 93
<211> 2115
<212> DNA
<213> Artificial Sequence

<220>
<223> pLSBC1773, see Example 14

<400> 93
gccggcatgc ttgatatcgt gatgacccag tctcacaaat tcatgtccac atcagtagga 60

gacagggtca gcatcacctg caaggccagt caggatgtga atactgctgt agcctggtat 120

caacagaaac caggacattc tccgaaacta ctgatttact cggcatcctt ccggtacact 180

ggagtccctg atcgcttcac tggcaataga tctgggacgg atttcacttt caccatcagc 240

agtgtgcagg ctgaagacct ggcagtttat tactgtcagc aacattatac tactcctccc 300

acgttcggag gggggaccaa gctggagata aaacgggctg atgctgcacc aactgtatcc 360

atcttcccac catccagtga gcagttaaca tctggaggtg cctcagtcgt gtgcttcttg 420

aacaacttct accccaaaga catcaatgtc aagtggaaga ttgatggcag tgaacgacaa 480

aatggcgtcc tgaacagttg gactgatcag gacagcaaag acagcaccta cagcatgagc 540

agcaccctca cgttgaccaa ggacgagtat gaacgacata acagctatac ctgtgaggcc 600

actcacaaga catcaacttc acccattgtc aagagcttca acaggaatga gtgtggaggt 660

aaacgtacga tacaggattc tgcaactgat acagttgact taggtgcaga gttgcataga 720

gatgaccctc cacctactgc ttctgatatc ggaaagcgag gcaagagggg aggtcaggtt 780

cagctgcagc agtctgggcc agagcttgtg aagccagggg cctcactcaa gttgtcctgt 840

acagcttctg gcttcaacat taaagacacc tatatacact gggtgaaaca gaggcctgaa 900

cagggcctgg aatggattgg aaggatttat cctacgaatg gttatactag atatgacccg 960

aagttccagg acaaggccac tataacagca gacacatcct ccaacacagc ctacctgcag 1020

gtcagccgcc tgacatctga ggacactgcc gtctattatt gttctagatg gggaggggac 1080

ggcttctatg ctatggacta ctggggtcaa ggagcctcag tcaccgtctc ctcagccaaa 1140

acgacacccc catctgtcta tccactggcc cctggrtctg ctgcccaaac taactccatg 1200

gtgaccctgg gatgcctggt caagggctat ttccctgagc cagtgacagt gacctggaac 1260

tctggatccc tgtccagcgg tgtgcacacc ttcccagctg tcctgcagtc tgacctctac 1320

actctgagca gctcagtgac tgtcccctcc agcacctggc ccagcgagac cgtcacctgc 1380

aacgttgccc acccggccag cagcaccaag gtggacaaga aaattgtgcc cagggattgt 1440

ggttgtaagc cttgcatatg tacagtccca gaagtatcat ctgtcttcat cttcccccca 1500

aagcccaagg atgtgctcac cattactctg actcctaagg tcacgtgtgt tgtggtagac 1560

```
atcagcaagg atgatcccga ggtccagttc agctggtttg tagatgatgt ggaggtgcac    1620

acagctcaga cgcaaccccg ggaggagcag ttcaacagca ctttccgctc agtcagtgaa    1680

cttcccatca tgcaccagga ctggctcaat gacaaggagt tcaaatgcag ggtcaacagt    1740

gcagctttcc ctgcccccat cgagaaaacc atctccaaaa ccaaaggcag accgaaggct    1800

ccacaggtgt acaccattcc acctcccaag gagcagatgg ccaaggataa agtcagtctg    1860

acctgcatga taacagactt cttccctgaa gacattactg tggagtggca gtggaatggg    1920

cagccagcgg agaactacaa gaacactcag cccatcatgg acacagatgg ctcttacttc    1980

gtctacagca agctcaatgt gcagaagagc aactgggagg caggaaatac tttcacctgc    2040

tctgtgttac atgagggcct gcacaaccac catactgaga agagcctctc ccactctcct    2100

ggtaaatgac ctagg                                                      2115
```

```
<210>  94
<211>  700
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  pLSBC1773, see Example 14

<400>  94

Met Leu Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser
1               5                   10                  15


Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Asn
            20                  25                  30


Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly His Ser Pro Lys Leu
        35                  40                  45


Leu Ile Tyr Ser Ala Ser Phe Arg Tyr Thr Gly Val Pro Asp Arg Phe
    50                  55                  60


Thr Gly Asn Arg Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val
65                  70                  75                  80


Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr Thr Thr
                85                  90                  95


Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp
            100                 105                 110


Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr
        115                 120                 125
```

```
Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys
    130                 135                 140

Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly
145                 150                 155                 160

Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser
                165                 170                 175

Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn
            180                 185                 190

Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val
        195                 200                 205

Lys Ser Phe Asn Arg Asn Glu Cys Gly Gly Lys Arg Thr Ile Gln Asp
    210                 215                 220

Ser Ala Thr Asp Thr Val Asp Leu Gly Ala Glu Leu His Arg Asp Asp
225                 230                 235                 240

Pro Pro Pro Thr Ala Ser Asp Ile Gly Lys Arg Gly Lys Arg Gly Gly
                245                 250                 255

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
            260                 265                 270

Ser Leu Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
        275                 280                 285

Tyr Ile His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
    290                 295                 300

Gly Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Asp Pro Lys Phe
305                 310                 315                 320

Gln Asp Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
                325                 330                 335

Leu Gln Val Ser Arg Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
            340                 345                 350

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
        355                 360                 365

Gly Ala Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
    370                 375                 380
```

```
Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
385                 390                 395                 400

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
                405                 410                 415

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
            420                 425                 430

Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
        435                 440                 445

Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala
    450                 455                 460

Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys
465                 470                 475                 480

Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe
                485                 490                 495

Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val
            500                 505                 510

Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe
        515                 520                 525

Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro
    530                 535                 540

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro
545                 550                 555                 560

Ile Met His Gln Asp Trp Leu Asn Asp Lys Glu Phe Lys Cys Arg Val
                565                 570                 575

Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
            580                 585                 590

Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys
        595                 600                 605

Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp
    610                 615                 620

Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro
```

```
625                 630                 635                 640


Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser
                645                 650                 655


Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala
            660                 665                 670


Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His
        675                 680                 685


His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
    690                 695                 700


<210>  95
<211>  172
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  pLSBC2268, see Example 9

<400>  95

Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Lys Ala Gly Ser Tyr
1               5                   10                  15


Ser Ile Thr Thr Pro Ser Gln Phe Val Phe Leu Ser Ser Ala Trp Ala
            20                  25                  30


Asp Pro Ile Glu Leu Ile Asn Leu Cys Thr Asn Ala Leu Gly Asn Gln
        35                  40                  45


Phe Gln Thr Gln Gln Ala Arg Thr Val Val Gln Arg Gln Phe Ser Glu
    50                  55                  60


Val Trp Lys Pro Ser Pro Gln Val Thr Val Arg Phe Pro Asp Ser Asp
65                  70                  75                  80


Phe Lys Val Tyr Arg Tyr Asn Ala Val Leu Asp Pro Leu Val Thr Ala
                85                  90                  95


Leu Leu Gly Ala Phe Asp Thr Arg Asn Arg Ile Ile Glu Val Glu Asn
            100                 105                 110


Gln Ala Asn Pro Thr Thr Ala Glu Thr Leu Asp Ala Thr Arg Arg Val
        115                 120                 125


Asp Asp Ala Thr Val Ala Ile Arg Ser Ala Ile Asn Asn Leu Ile Val
    130                 135                 140
```

```
Glu Leu Ile Arg Gly Thr Gly Ser Tyr Asn Arg Ser Ser Phe Glu Ser
145                 150                 155                 160


Ser Ser Gly Leu Val Trp Thr Ser Gly Pro Ala Thr
                165                 170


<210>  96
<211>  708
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  pLSB2634, see Example 23

<400>  96
aatagctgtg aattgactaa tatcacgata gcaatcgaga aggaagagtg tagattctgt      60

atatctataa atactacgtg gtgtgcaggt tactgttata ctagggactt agtttacaaa     120

gaccctgcca gacctaaaat acaaaaaact tgtactttca aagaattagt ttacgaaact     180

gttagagtgc caggttgtgc acatcacgca gactcattat acacttaccc tgtggcaact     240

caatgtcatt gtggtaaatg tgactctgac tctactgact gtactgtgag aggtttagga     300

ccatcttact gttctttcgg agaaatgaag gagaaaagaa ctatacaaga ctctgcaacg     360

gacacggtgg acttaggagc tgaattacat agggacgatc ctccacctac tgcatcagac     420

ataggaaaaa gggctcctga tgtgcaggat tgcccagaat gcacgctaca ggaaaaccca     480

ttcttctccc agccgggtgc cccaatactt cagtgcatgg gctgctgctt ctctagagca     540

tatcccactc cactaaggtc caagaagacg atgttggtcc aaaagaacgt cacctcagag     600

tccacttgct gtgtagctaa atcatataac agggtcacag taatgggggg tttcaaagtg     660

gagaaccaca cggcgtgcca ctgcagtact tgttattatc acaaatct                  708


<210>  97
<211>  236
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  pLSB2634, see Example 23

<400>  97

Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys Glu Glu
1               5                   10                  15


Cys Arg Phe Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys
            20                  25                  30


Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln
```

```
        35                  40                  45


Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg Val Pro
    50                  55                  60


Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val Ala Thr
65                  70                  75                  80


Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys Thr Val
                85                  90                  95


Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys Glu Lys
            100                 105                 110


Arg Thr Ile Gln Asp Ser Ala Thr Asp Thr Val Asp Leu Gly Ala Glu
        115                 120                 125


Leu His Arg Asp Asp Pro Pro Pro Thr Ala Ser Asp Ile Gly Lys Arg
    130                 135                 140


Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro
145                 150                 155                 160


Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys
                165                 170                 175


Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu
            180                 185                 190


Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser
        195                 200                 205


Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His Thr
    210                 215                 220


Ala Cys His Cys Ser Thr Cys Tyr Tyr His Lys Ser
225                 230                 235


<210>  98
<211>  60
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  KP509, see Example 23

<400>  98
gcaatcgaga aggaagagtg tagattctgt atatctataa atactacgtg gtgtgcaggt      60
```

```
<210>  99
<211>  60
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  KP510, see Example 23

<400>  99
tactgttata ctagggactt agtttacaaa gaccctgcca gacctaaaat acaaaaaact      60


<210>  100
<211>  60
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  KP511, see Example 23

<400>  100
tgtactttca aagaattagt ttacgaaact gttagagtgc caggttgtgc acatcacgca      60


<210>  101
<211>  60
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  KP512, see Example 23

<400>  101
gactcattat acacttaccc tgtggcaact caatgtcatt gtggtaaatg tgactctgac      60


<210>  102
<211>  60
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  KP513, see Example 23

<400>  102
tctactgact gtactgtgag aggtttagga ccatcttact gttctttcgg agaaatgaag      60


<210>  103
<211>  60
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  KP514, see Example 23

<400>  103
gagaaaagaa ctatacaaga ctctgcaacg gacacggtgg acttaggagc tgaattacat      60


<210>  104
<211>  59
<212>  DNA
```

```
<213>  Artificial Sequence

<220>
<223>  KP515, see Example 23

<400>  104
agagccggca atagctgtga attgactaat atcacgatag caatcgagaa ggaagagtg      59


<210>  105
<211>  22
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  KP516, see Example 23

<400>  105
ataggaaaaa gggctcctga tg                                              22


<210>  106
<211>  60
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  KP517, see Example 23

<400>  106
cgttgcagag tcttgtatag ttcttttctc cttcatttct ccgaaagaac agtaagatgg     60


<210>  107
<211>  60
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  KP518, see Example 23

<400>  107
tcctaaacct ctcacagtac agtcagtaga gtcagagtca catttaccac aatgacattg     60


<210>  108
<211>  60
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  KP519, see Example 23

<400>  108
agttgccaca gggtaagtgt ataatgagtc tgcgtgatgt gcacaacctg gcactctaac     60


<210>  109
<211>  60
<212>  DNA
<213>  Artificial Sequence

<220>
```

```
<223>  KP520, See Example 23

<400>  109
agtttcgtaa actaattctt tgaaagtaca agttttttgt attttaggtc tggcagggtc      60


<210>  110
<211>  60
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  KP521, see Example 23

<400>  110
tttgtaaact aagtccctag tataacagta acctgcacac cacgtagtat ttatagatat      60


<210>  111
<211>  52
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  KP522, see Example 23

<400>  111
gtctgatgca gtaggtggag gatcgtccct atgtaattca gctcctaagt cc              52


<210>  112
<211>  43
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  KP523, see Example 23

<400>  112
agactcgagc ctaggctaag atttgtgata ataacaagta ctg                        43


<210>  113
<211>  55
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  KP524

<400>  113
agactcgagc ctaggctata attcgtcatg agatttgtga taataacaag tactg           55


<210>  114
<211>  42
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  KP525

<400>  114
```

ctccacctac tgcatcagac ataggaaaaa gggctcctga tg 42

<210> 115
<211> 2147
<212> DNA
<213> Artificial Sequence

<220>
<223> pLSBC1799, see Example 5

<400> 115
gcatgctaga cattgtgctg acccaatctc cagcttcttt ggctgtatct ctaggacaga 60

gggccaccat ctcctgcaga gccagcgaaa gtgttgataa ttatggcttt agttttatga 120

actggttcca acagaaacca ggacagccac ccaaactcct catctatgct atatccaacc 180

gaggatccgg ggtccctgcc aggtttagtg gcagtgggtc tgggacagac ttcagcctca 240

acatccatcc tgtagaggag gatgatcctg caatgtattt ctgtcagcaa actaaggagg 300

ttccgtggac gttcggtgga ggcaccaagc tggaaatcaa acgggctgat gctgcaccaa 360

ctgtatccat cttcccacca tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt 420

gcttcttgaa caacttctac cccaaagaca tcaatgtcaa gtggaagatt gatggcagtg 480

aacgacaaaa tggcgtcctg aacagttgga ctgatcagga cagcaaagac agcacctaca 540

gcatgagcag caccctcacg ttgaccaagg acgagtatga acgacataac agctatacct 600

gtgaggccac tcacaagaca tcaacttcac ccattgtcaa gagcttcaac aggaatgagt 660

gtggaggtaa acgtacgata caggattctg caactgatac agttgactta ggtgcagagt 720

tgcatagaga tgaccctcca cctactgctt ctgatatcgg aaagcgaggc aagaggggag 780

gtgaagtaga tctggttgag tctgggggag acttagtgaa gcctggaggg tccctgaaac 840

tctcctgtgc agcctctgga ttcactttca gtcactatgg catgtcttgg gttcgccaga 900

ctccagacaa gaggctggag tgggtcgcaa ccattggtag tcgtggtact tacacccact 960

atccagacag tgtgaaggga cgattcacca tctccagaga caatgacaag aacgccctgt 1020

acctgcaaat gaacagtctg aagtgtgaag acacagccat gtattactgt gcaagaagaa 1080

gtgaatttta ttactacggt aatacctact attactctgc tatggactac tggggtcaag 1140

gagcctcagt caccgtctcc tcagccaaaa cgacaccccc atctgtctat ccactggccc 1200

ctggatctgc tgcccaaact aactccatgg tgaccctggg atgcctggtc aagggctatt 1260

tccctgagcc agtgacagtg acctggaact ctggatccct gtccagcggt gtgcacacct 1320

tcccagctgt cctgcagtct gacctccaca ctctgagcag ctcagtgact gtcccctcca 1380

gcacctggcc cagcgagacc gtcacctgca acgttgccca cccggccagc agcaccaagg 1440

tggacaagaa aattgtgccc agggattgtg gttgtaagcc ttgcatatgt acagtcccag 1500

aagtatcatc tgtcttcatc ttccccccaaa agcccaagga tgtgctcacc attactctga 1560 ctcctaaggt cacgtgtgtt gtggtagaca tcagcaagga tgatcccgag gtccagttca 1620

gctggtttgt agatgatgtg gaggtgcaca cagctcagac gcaaccccgg gaggagcagt 1680

tcaacagcac tttccgctca gtcagtggaa cttcccatca tgcaccaagg actgggctca 1740

atgacaagga gttcaaatgc agggtcaaca gtgcagcttt ccctgccccc atcgagaaaa 1800

ccatctccaa aaccaaaggc agaccgaagg ctccacaggt gtacaccatt ccacctccca 1860

aggagcagat ggccaaggat aaagtcagtc tgacctgcat gataacagac ttcttccctg 1920

aagacattac tgtggagtgg cagtggaatg ggcagccagc ggagaactac aagaacactc 1980

agcccatcat ggacacagat ggctcttact tcgtctacag caagctcaat gtgcagaaga 2040

gcaactggga ggcaggaaat actttcacct gctctgtgtt acatgagggc ctgcacaacc 2100

accatactga gaagagcctc tcccactctc ctggtaaatg acctagg 2147

<210> 116
<211> 712
<212> PRT
<213> Artificial Sequence

<220>
<223> pLSBC1799, see Example 5

<400> 116

```
Met Leu Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser
1               5                   10                  15


Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp
            20                  25                  30


Asn Tyr Gly Phe Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln
        35                  40                  45


Pro Pro Lys Leu Leu Ile Tyr Ala Ile Ser Asn Arg Gly Ser Gly Val
    50                  55                  60


Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn
65                  70                  75                  80


Ile His Pro Val Glu Glu Asp Asp Pro Ala Met Tyr Phe Cys Gln Gln
                85                  90                  95


Thr Lys Glu Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
            100                 105                 110


Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser
        115                 120                 125
```

```
Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu
145                 150                 155                 160

Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr
            180                 185                 190

Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr
        195                 200                 205

Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys Gly Gly Lys Arg
    210                 215                 220

Thr Ile Gln Asp Ser Ala Thr Asp Thr Val Asp Leu Gly Ala Glu Leu
225                 230                 235                 240

His Arg Asp Asp Pro Pro Pro Thr Ala Ser Asp Ile Gly Lys Arg Gly
                245                 250                 255

Lys Arg Gly Gly Glu Val Asp Leu Val Glu Ser Gly Gly Asp Leu Val
            260                 265                 270

Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
        275                 280                 285

Phe Ser His Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg
    290                 295                 300

Leu Glu Trp Val Ala Thr Ile Gly Ser Arg Gly Thr Tyr Thr His Tyr
305                 310                 315                 320

Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Asp Lys
                325                 330                 335

Asn Ala Leu Tyr Leu Gln Met Asn Ser Leu Lys Cys Glu Asp Thr Ala
            340                 345                 350

Met Tyr Tyr Cys Ala Arg Arg Ser Glu Phe Tyr Tyr Tyr Gly Asn Thr
        355                 360                 365

Tyr Tyr Tyr Ser Ala Met Asp Tyr Trp Gly Gln Gly Ala Ser Val Thr
    370                 375                 380
```

```
Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro
385                 390                 395                 400

Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val
                405                 410                 415

Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser
            420                 425                 430

Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu
        435                 440                 445

His Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser
    450                 455                 460

Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val
465                 470                 475                 480

Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys
                485                 490                 495

Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Gln Lys Pro Lys
            500                 505                 510

Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val
        515                 520                 525

Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp
    530                 535                 540

Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe
545                 550                 555                 560

Asn Ser Thr Phe Arg Ser Val Ser Gly Thr Ser His His Ala Pro Arg
                565                 570                 575

Thr Gly Leu Asn Asp Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala
            580                 585                 590

Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro
        595                 600                 605

Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala
    610                 615                 620

Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu
```

625 630 635 640

Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr
645 650 655

Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr
660 665 670

Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe
675 680 685

Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys
690 695 700

Ser Leu Ser His Ser Pro Gly Lys
705 710

<210> 117
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> pLSBC2523 , see Example 6

<400> 117
gaggtaaagc tggagcagtc tggcgctgag ttggtgaaac ctggggcttc agtgaagata 60

tcctgcaagg cttctggcta caccttcact gaccatgtta ttcactgggt gaagcagagg 120

cctgaacagg gcctggaatg gattggattt atttctcccg gaaatggtga tattagatat 180

aatgagaagt tcaaggacaa ggccacactg actgcagaca aatcctccag cactgcctac 240

atgcagctca atagtctgac atctgaggat tctgcagtgt atttctgtaa gagatccttt 300

tattactacg atgataacta cggggactac tggggccaag gcaccactct cacagtctcc 360

tcagccaaaa caacagcccc atcggtctat ccactggccc ctgtgtgtgg agatacaagt 420

ggctcctcgg tgactctagg atgcctggtc aagggttatt tccctgagcc agtgaccttg 480

acctggaact ctggatccct gtccagtggt gtgcacacct tcccagctgt cctgcagtct 540

gacctctaca ccctcagcag ctcagtgact gtaacctcga gcacctggcc cagccagtcc 600

atcacctgca atgtggccca cccggcaagc agcaccaagg tggacaagaa aattgagccc 660

agagggccca caatcaagcc ctgtcctcca tgcaaatgcc cagcacctaa cctcttgggt 720

ggaccatccg tcttcatctt ccctccaaag atcaaggatg tactcatgat ctccctgagc 780

cccatagtca catgtgtggt ggtggatgtg agcgaggatg acccagatgt ccagatcagc 840

tggtttgtga acaacgtgga agtacacaca gctcagacac aaacccatag agaggattac 900

aacagtactc tccgggtggt cagtgccctc cccatccagc accaggactg gatgagtggc 960

```
aaggagttca aatgcaaggt caacaacaaa gacctcccag cgcccatcga gagaaccatc    1020

tcaaaaccca aagggtcagt aagagctcca caggtatatg tcttgcctcc accagaagaa    1080

gagatgacta agaaacaggt cactctgacc tgcatggtca cagacttcat gcctgaagac    1140

atttacgtgg agtggaccaa caacgggaaa acagagctaa actacaagaa cactgaacca    1200

gtcctggact ctgatggttc ttacttcatg tacagcaagc tgagagtgga aaagaagaac    1260

tgggtggaaa gaaatagcta ctcctgttca gtggtccacg agggtctgca caatcaccac    1320

acgactaaga gcttctccca ctctcctggt aaatga                              1356


<210>  118
<211>  451
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  pLSBC2523 , see Example 6

<400>  118

Glu Val Lys Leu Glu Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20                  25                  30


Val Ile His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Phe Ile Ser Pro Gly Asn Gly Asp Ile Arg Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80


Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95


Lys Arg Ser Phe Tyr Tyr Tyr Asp Asp Asn Tyr Gly Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Ala Pro Ser
        115                 120                 125


Val Tyr Pro Leu Ala Pro Val Cys Gly Asp Thr Ser Gly Ser Ser Val
    130                 135                 140


Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu
```

145 150 155 160

Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr
180 185 190

Ser Ser Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro
195 200 205

Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr
210 215 220

Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly
225 230 235 240

Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met
245 250 255

Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu
260 265 270

Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val
275 280 285

His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu
290 295 300

Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly
305 310 315 320

Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile
325 330 335

Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val
340 345 350

Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr
355 360 365

Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu
370 375 380

Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro
385 390 395 400

```
Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val
                405                 410                 415


Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val
            420                 425                 430


His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser His Ser
        435                 440                 445


Pro Gly Lys
    450


<210>  119
<211>  648
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  pLSBC1757, see Example 6

<400>  119
caaattgttc tcacccagtc tccagcaatc atgtctgcat ctctagggga acgggtcacc      60

atgacctgca ctgccagctc aagtgtaagt tccagttact tccactggta ccagcagaag     120

ccaggatcct cccccaaact ctggatttat accacatcca acctggcttc tggagtccca     180

gctcgcttca gtggcagtgg gtctgggacc tcttactctc tcacaatcag cagcatggag     240

gctgaagatg ctgccactta ttactgccac cagtatcatc gttccccgct cacgttcggt     300

gctgggacca agctggagct gaaacgggct gatgctgcac caactgtatc catcttccca     360

ccatccagtg agcagttaac atctggaggt gcctcagtcg tgtgcttctt gaacaacttc     420

taccccaaag acatcaatgt caagtggaag attgatggca gtgaacgaca aaatggcgtc     480

ctgaacagtt ggactgatca ggacagcaaa gacagcacct acagcatgag cagcaccctc     540

acgttgacca aggacgagta tgaacgacat aacagctata cctgtgaggc cactcacaag     600

acatcaactt cacccattgt caagagcttc aacaggaatg agtgttag                  648


<210>  120
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  pLSBC1757, see Example 6

<400>  120

Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Leu Gly
1               5                   10                  15


Glu Arg Val Thr Met Thr Cys Thr Ala Ser Ser Ser Val Ser Ser Ser
```

```
            20                  25                  30

Tyr Phe His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Leu Trp
        35                  40                  45

Ile Tyr Thr Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu
65                  70                  75                  80

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Tyr His Arg Ser Pro
                85                  90                  95

Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala
            100                 105                 110

Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser
        115                 120                 125

Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp
    130                 135                 140

Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val
145                 150                 155                 160

Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met
                165                 170                 175

Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser
            180                 185                 190

Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys
        195                 200                 205

Ser Phe Asn Arg Asn Glu Cys
    210                 215


<210>  121
<211>  1458
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  pLSBC1792, see Example 6

<400>  121
gccggccaaa ttgttctcac ccagtctcca gcaatcatgt ctgcatctct aggggaacgg      60

gtcaccatga cctgcactgc cagctcaagt gtaagttcca gttacttcca ctggtaccag     120
```

cagaagccag gatcctcccc caaactctgg atttatacca catccaacct ggcttctgga 180

gtcccagctc gcttcagtgg cagtgggtct gggacctctt actctctcac aatcagcagc 240

atggaggctg aagatgctgc cacttattac tgccaccagt atcatcgttc cccgctcacg 300

ttcggtgctg ggaccaagct ggagctgaaa cgggctgatg ctgcaccaac tgtatccatc 360

ttcccaccat ccagtgagca gttaacatct ggaggtgcct cagtcgtgtg cttcttgaac 420

aacttctacc ccaaagacat caatgtcaag tggaagattg atggcagtga acgacaaaat 480

ggcgtcctga acagttggac tgatcaggac agcaaagaca gcacctacag catgagcagc 540

accctcacgt tgaccaagga cgagtatgaa cgacataaca gctatacctg tgaggccact 600

cacaagacat caacttcacc cattgtcaag agcttcaaca ggaatgagtg tggaggtaaa 660

cgtacgatac aggattctgc aactgataca gttgacttag gtgcagagtt gcatagagat 720

gaccctccac ctactgcttc tgatatcgga aagcgaggca agaggggagg tgaggtaaag 780

ctggaggagt ctggcgctga gttggtgaaa cctggggctt cagtgaagat atcctgcaag 840

gcttctggct acaccttcac tgaccatgtt attcactggg tgaagcagag gcctgaacag 900

ggcctggaat ggattggatt tatttctccc ggaaatggtg atattagata taatgagaag 960

ttcaaggaca aggccacact gactgcagac aaatcctcca gcactgccta catgcagctc 1020

aatagtctga catctgagga ttctgcagtg tatttctgta agagatcctt ttattactac 1080

gatgataact acggggacta ctggggccaa ggcaccactc tcacagtctc ctcagccaaa 1140

acaacagccc catcggtcta tccactggcc cctgtgtgtg gagatacaag tggctcctcg 1200

gtgactctag gatgcctggt caagggttat ttccctgagc cagtgacctt gacctggaac 1260

tctggatccc tgtccagtgg tgtgcacacc ttcccagctg tcctgcagtc tgacctctac 1320

accctcagca gctcagtgac tgtaacctcg agcacctggc ccagccagtc catcacctgc 1380

aatgtggccc acccggcaag cagcaccaag gtggacaaga aaattgagcc cagagggccc 1440

acaatcaagc cctgttga 1458

<210> 122
<211> 483
<212> PRT
<213> Artificial Sequence

<220>
<223> pLSBC1792, see Example 6

<400> 122

Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Leu Gly
1 5 10 15

Glu Arg Val Thr Met Thr Cys Thr Ala Ser Ser Ser Val Ser Ser Ser

```
            20                  25                  30

Tyr Phe His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Leu Trp
        35                  40                  45

Ile Tyr Thr Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu
65                  70                  75                  80

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Tyr His Arg Ser Pro
                85                  90                  95

Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala
            100                 105                 110

Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser
        115                 120                 125

Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp
    130                 135                 140

Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val
145                 150                 155                 160

Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met
                165                 170                 175

Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser
            180                 185                 190

Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys
        195                 200                 205

Ser Phe Asn Arg Asn Glu Cys Gly Gly Lys Arg Thr Ile Gln Asp Ser
    210                 215                 220

Ala Thr Asp Thr Val Asp Leu Gly Ala Glu Leu His Arg Asp Asp Pro
225                 230                 235                 240

Pro Pro Thr Ala Ser Asp Ile Gly Lys Arg Gly Lys Arg Gly Gly Glu
                245                 250                 255

Val Lys Leu Glu Glu Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
            260                 265                 270
```

```
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His Val
        275                 280                 285

Ile His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
    290                 295                 300

Phe Ile Ser Pro Gly Asn Gly Asp Ile Arg Tyr Asn Glu Lys Phe Lys
305                 310                 315                 320

Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met
                325                 330                 335

Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Lys
            340                 345                 350

Arg Ser Phe Tyr Tyr Tyr Asp Asp Asn Tyr Gly Asp Tyr Trp Gly Gln
        355                 360                 365

Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Ala Pro Ser Val
    370                 375                 380

Tyr Pro Leu Ala Pro Val Cys Gly Asp Thr Ser Gly Ser Ser Val Thr
385                 390                 395                 400

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr
                405                 410                 415

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
            420                 425                 430

Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser
        435                 440                 445

Ser Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro Ala
    450                 455                 460

Ser Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile
465                 470                 475                 480

Lys Pro Cys
```